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(54) Title: NON-ENDOGENOUS, CONSTITUTIVELY ACTIVATED HUMAN SEROTONIN RECEPTORS AND SMALL MOLECULE MODULATORS THEREOF			
(57) Abstract			
Disclosed herein are non-endogenous, constitutively activated forms of the human 5-HT _{2A} and human 5-HT _{2C} receptors and uses of such receptors to screen candidate compounds. Further disclosed herein are candidate compounds identified by the screening method which act at the 5HT _{2A} receptors. Yet further disclosed is a new class of compounds which act at the 5HT _{2A} receptors.			

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**NON-ENDOGENOUS, CONSTITUTIVELY ACTIVATED
HUMAN SEROTONIN RECEPTORS AND SMALL
MOLECULE MODULATORS THEREOF**

5 The benefit of U.S. Serial Number 09/060,188, filed April 14, 1998 (owned by Arena Pharmaceuticals, Inc.) and U.S. Provisional Number 60/090,783, filed June 26, 1998 (owned by Arena Pharmaceuticals), U.S. Provisional Number 60/112,909, filed December 18, 1998, and U.S. Provisional Number 60/123,000 filed March 5, 1999 is hereby claimed.

10 **FIELD OF THE INVENTION**

 The present invention relates to non-endogenous, constitutively active serotonin receptors and small molecule modulators thereof.

BACKGROUND OF THE INVENTION

15 **I. G protein-coupled receptors**

 G protein-coupled receptors share a common structural motif. All these receptors have seven sequences of between 22 to 24 hydrophobic amino acids that form seven alpha helices, each of which spans the membrane. The transmembrane helices are joined by strands of amino
20 acids having a larger loop between the fourth and fifth transmembrane helix on the extracellular side of the membrane. Another larger loop, composed primarily of hydrophilic amino acids, joins transmembrane helices five and six on the intracellular side of the membrane. The carboxy terminus of the receptor lies intracellularly with the amino terminus in the extracellular space. It is thought that the loop joining helices five and six, as well as, the
25 carboxy terminus, interact with the G protein. Currently, Gq, Gs, Gi, and Go are G proteins that have been identified. The general structure of G protein-coupled receptors is shown in Figure 1.

 Under physiological conditions, G protein-coupled receptors exist in the cell membrane in equilibrium between two different states or conformations: an "inactive" state and an
30 "active" state. As shown schematically in Figure 2, a receptor in an inactive state is unable to link to the intracellular transduction pathway to produce a biological response. Changing the receptor conformation to the active state allows linkage to the transduction pathway and produces a biological response.

A receptor may be stabilized in an active state by an endogenous ligand or an exogenous agonist ligand. Recent discoveries such as, including but not exclusively limited to, modifications to the amino acid sequence of the receptor provide means other than ligands to stabilize the active state conformation. These means effectively stabilize the receptor in an active state by simulating the effect of a ligand binding to the receptor. Stabilization by such ligand-independent means is termed "constitutive receptor activation."

II. Serotonin receptors

Receptors for serotonin (5-hydroxytryptamine, 5-HT) are an important class of G protein-coupled receptors. Serotonin is thought to play a role in processes related to learning and memory, sleep, thermoregulation, mood, motor activity, pain, sexual and aggressive behaviors, appetite, neurodegenerative regulation, and biological rhythms. Not surprisingly, serotonin is linked to pathophysiological conditions such as anxiety, depression, obsessive-compulsive disorders, schizophrenia, suicide, autism, migraine, emesis, alcoholism and neurodegenerative disorders.

Serotonin receptors are divided into seven subfamilies, referred to as 5-HT1 through 5-HT7, inclusive. These subfamilies are further divided into subtypes. For example, the 5-HT2 subfamily is divided into three receptor subtypes: 5-HT2A, 5-HT2B, and 5-HT2C. The human 5-HT2C receptor was first isolated and cloned in 1987, and the human 5-HT2A receptor was first isolated and cloned in 1990. These two receptors are thought to be the site of action of hallucinogenic drugs. Additionally, antagonists to the 5-HT2A and 5-HT2C receptors are believed to be useful in treating depression, anxiety, psychosis and eating disorders.

U.S. Patent Number 4,985,352, describes the isolation, characterization, and expression of a functional cDNA clone encoding the entire human 5-HT1C receptor (now known as the 5HT2C receptor). U.S. Patent Number 5,661,0124 describes the isolation, characterization, and expression of a functional cDNA clone encoding the entire human 5-HT2A receptor.

Mutations of the endogenous forms of the rat 5-HT2A and rat 5-HT2C receptors have been reported to lead to constitutive activation of these receptors (5-HT2A: Casey, C. *et al.* (1996) *Society for Neuroscience Abstracts*, 22:699.10, hereinafter "Casey"; 5-HT2C: Herrick-Davis, K., and Teitler, M. (1996) *Society for Neuroscience Abstracts*, 22:699.18, hereinafter "Herrick-Davis 1"; and Herrick-Davis, K. *et al.* (1997) *J.Neurochemistry* 69(3): 1138, hereinafter "Herrick-Davis-2"). Casey describes a mutation of the cysteine residue at position 322 of the rat 5-HT2A receptor to lysine (C322K), glutamine (C322Q) and arginine (C322R) which reportedly led to constitutive activation. Herrick-Davis 1 and Herrick-Davis 2 describe

mutations of the serine residue at position 312 of the rat 5-HT_{2C} receptor to phenylalanine (S312F) and lysine (S312K), which reportedly led to constitutive activation.

SUMMARY OF THE INVENTION

5 The present invention relates to non-endogenous, constitutively activated forms of the human 5-HT_{2A} and human 5-HT_{2C} receptors and various uses of such receptors. Further disclosed are small molecule modulators of these receptors. Most preferably, these modulators have inverse agonist characteristics at the receptor.

10 More specifically, the present invention discloses nucleic acid molecules and the proteins for three non-endogenous, constitutively activated human serotonin receptors, referred to herein as, AP-1, AP-3, and AP-4. The AP-1 receptor is a constitutively active form of the human 5-HT_{2C} receptor created by an S310K point mutation. The AP-3 receptor is a constitutively active form of the human 5-HT_{2A} receptor whereby the intracellular loop 3 (IC3) portion and the cytoplasmic-tail portion of the endogenous human 5-HT_{2A} receptor have
15 been replaced with the IC3 portion and the cytoplasmic-tail portion of the human 5-HT_{2C} receptor. The AP-4 receptor is a constitutively active form of the human 5-HT_{2A} receptor whereby (1) the region of the intracellular third loop between the proline of the transmembrane 5 region (TM5) and the proline of TM6 of the endogenous human 5-HT_{2A} receptor has been replaced with the corresponding region of the human 5-HT_{2C} receptor (including a S310K
20 point mutation); and (2) the cytoplasmic-tail portion of the endogenous human 5-HT_{2A} receptor has been replaced with the cytoplasmic-tail portion of the endogenous human 5-HT_{2C} receptor.

The invention also provides assays that may be used to directly identify candidate compounds as agonists, partial agonists or inverse agonists to non-endogenous, constitutively
25 activated human serotonin receptors; such candidate compounds can then be utilized in pharmaceutical composition(s) for treatment of diseases and disorders which are related to the human 5-HT_{2A} and/or human 5-HT_{2C} receptors.

These and other aspects of the invention disclosed herein will be set forth in greater detail as the patent disclosure proceeds.

BRIEF DESCRIPTION OF THE DRAWINGS

30 In the following figures, bold typeface indicates the location of the mutation in the non-endogenous, constitutively activated receptor relative to the corresponding endogenous receptor.

Figure 1 shows a generalized structure of a G protein-coupled receptor with the numbers assigned to the transmembrane helices, the intracellular loops, and the extracellular loops.

Figure 2 schematically shows the active and inactive states for a typical G protein-coupled receptor and the linkage of the active state to the second messenger transduction pathway.

Figure 3a provides the nucleic acid sequence of the endogenous human 5-HT2A receptor (SEQ.ID.NO: 24).

Figure 3b provides the corresponding amino acid sequence of the endogenous human 5-HT2A receptor (SEQ.ID.NO: 25).

Figure 4a provides the nucleic acid sequence of the endogenous human 5-HT2C receptor (SEQ.ID.NO: 26).

Figure 4b provides the corresponding amino acid sequence of the endogenous human 5-HT2C receptor (SEQ.ID.NO: 27).

Figure 5a provides the nucleic acid sequence of a constitutively active form of the human 5-HT2C receptor ("AP-1 cDNA" – SEQ.ID.NO: 28).

Figure 5b provides the corresponding amino acid sequence of the AP-1 cDNA ("AP-1" – SEQ.ID.NO: 29).

Figure 6a provides the nucleic acid sequence of a constitutively active form of the human 5-HT2A receptor whereby the IC3 portion and the cytoplasmic-tail portion of the endogenous 5-HT2A receptor have been replaced with the IC3 portion and the cytoplasmic-tail portion of the human 5-HT2C receptor ("AP-3 cDNA" – SEQ.ID.NO: 30).

Figure 6b provides the corresponding amino acid sequence of the AP-3 cDNA ("AP-3" – SEQ.ID.NO: 31).

Figure 6c provides a schematic representation of AP-3, where the dashed-lines represent the portion obtained from the human 5-HT2C receptor.

Figure 7a provides the nucleic acid sequence of a constitutively active form of the human 5-HT2A receptor whereby (1) the region of the between the proline of TM5 and the proline of TM6 of the endogenous human 5-HT2A receptor has been replaced with the corresponding region of the human 5-HT2C receptor (including a S310K point mutation); and (2) the cytoplasmic-tail portion of the endogenous 5-HT2A receptor has been replaced with the cytoplasmic-tail portion of the endogenous human 5-HT2C receptor ("AP-4 cDNA" – SEQ.ID.NO:32).

Figure 7b provides the corresponding amino acid sequence of the AP-4 cDNA ("AP-4" – SEQ.ID.NO: 33).

Figure 7c provides a schematic representation of the mutated 5-HT_{2A} receptor of Figure 7b where the dashed-lines represent the portion obtained from the human 5-HT_{2C} receptor.

Figure 8 is a representation of the preferred vector, pCMV, used herein.

Figure 9 is a diagram illustrating (1) enhanced [³⁵S]GTPγS binding to membranes prepared from COS cells expressing the endogenous human 5-HT_{2C} receptor in response to serotonin, and (2) inhibition by mianserin using wheatgerm agglutinin scintillation proximity beads. The concentration of [³⁵S]GTPγS was held constant at 0.3 nM, and the concentration of GDP was held at 1 μM. The concentration of the membrane protein was 12.5 μg.

Figure 10 is a diagram showing serotonin stimulation of [³⁵S]GTPγS binding to membranes expressing AP-1 receptors in 293T cells and the inhibition by 30 μM mianserin on Wallac™ scintistrips.

Figure 11 is a diagram showing the effects of protein concentration on [³⁵S]GTPγS binding in membranes prepared from 293T cells transfected with the endogenous human 5-HT_{2C} receptors and AP-1 receptors compared to cells transfected with the control vector (pCMV) alone in the absence (A) and presence (B) of 10 μM serotonin. The radiolabeled concentration of [³⁵S]GTPγS was held constant at 0.3 nM, and the GDP concentration was held constant at 1 μM. The assay was performed on 96-well format on Wallac™ scintistrips.

Figure 12 provides bar-graph comparisons of inositol trisphosphate ("IP₃") production between the endogenous human 5HT_{2A} receptor and AP-2, a mutated form of the receptor.

Figure 13 provides bar-graph comparisons of inositol trisphosphate ("IP₃") production between the endogenous human 5HT_{2A} receptor and AP-4, a mutated form of the receptor.

Figure 14 provides bar graph comparisons of IP₃ production between the endogenous human 5-HT_{2A} receptor and AP-3, a mutated form of the receptor.

Figure 15 provides bar-graph comparisons of IP₃ production between the endogenous human 5-HT_{2C} receptor and AP-1.

Figures 16A-C provides representative autoradiograms showing displacement of I¹²⁵-LSD from brain sections by spiperone and compound 116100.

Figure 17 shows in vivo response of animals to 116102 exposure.

DEFINITIONS

The scientific literature that has evolved around receptors has adopted a number of terms to refer to ligands having various effects on receptors. For clarity and consistency, the following definitions will be used throughout this patent document. To the extent that these definitions conflict with other definitions for these terms, the following definitions shall control.

AGONISTS shall mean moieties that activate the intracellular response when they bind to the receptor, or enhance GTP binding to membranes.

AMINO ACID ABBREVIATIONS used herein are set out in Table 1:

TABLE 1

ALANINE	ALA	A
ARGININE	ARG	R
ASPARAGINE	ASN	N
ASPARTIC ACID	ASP	D
CYSTEINE	CYS	C
GLUTAMIC ACID	GLU	E
GLUTAMINE	GLN	Q
GLYCINE	GLY	G
HISTIDINE	HIS	H
ISOLEUCINE	ILE	I
LEUCINE	LEU	L
LYSINE	LYS	K
METHIONINE	MET	M
PHENYLALANINE	PHE	F
PROLINE	PRO	P

SERINE	SER	S
THREONINE	THR	T
TRYPTOPHAN	TRP	W
TYROSINE	TYR	Y
VALINE	VAL	V

PARTIAL AGONISTS shall mean moieties which activate the intracellular response when they bind to the receptor to a lesser degree/extent than do agonists, or enhance GTP binding to membranes to a lesser degree/extent than do agonists.

5 **ANTAGONIST** shall mean moieties that competitively bind to the receptor at the same site as the agonists but which do not activate the intracellular response initiated by the active form of the receptor, and can thereby inhibit the intracellular responses by agonists or partial agonists. **ANTAGONISTS** do not diminish the baseline intracellular response in the absence of an agonist or partial agonist.

10 **CANDIDATE COMPOUND** shall mean a molecule (for example, and not limitation, a chemical compound) which is amenable to a screening technique.

COMPOUND EFFICACY shall mean a measurement of the ability of a compound to inhibit or stimulate receptor functionality, as opposed to receptor binding affinity.

15 **CONSTITUTIVELY ACTIVATED RECEPTOR** shall mean a receptor subject to constitutive receptor activation.

CONSTITUTIVE RECEPTOR ACTIVATION shall mean stabilization of a receptor in the active state by means other than binding of the receptor with its endogenous ligand or a chemical equivalent thereof.

20 **CONTACT** or **CONTACTING** shall mean bringing at least two moieties together, whether in an in vitro system or an in vivo system.

ENDOGENOUS shall mean a material that a mammal naturally produces. **ENDOGENOUS** in reference to, for example and not limitation, the term "receptor" shall mean that which is naturally produced by a mammal (for example, and not limitation, a human) or a virus.

25 In contrast, the term **NON-ENDOGENOUS** in this context shall mean that which is not naturally produced by a mammal (for example, and not limitation, a human) or a virus. For

example, and not limitation, a receptor which is not constitutively active in its endogenous form, but when manipulated becomes constitutively active, is most preferably referred to herein as a “non-endogenous, constitutively activated receptor.” Both terms can be utilized to describe both “in vivo” and “in vitro” systems. For example, and not a limitation, in a screening approach, the endogenous or non-endogenous receptor may be in reference to an in vitro screening system. As a further example and not limitation, where the genome of a mammal has been manipulated to include a non-endogenous constitutively activated receptor, screening of a candidate compound by means of an in vivo system is viable.

INHIBIT or **INHIBITING**, in relationship to the term “response” shall mean that a response is decreased or prevented in the presence of a compound as opposed to in the absence of the compound.

INVERSE AGONISTS shall mean moieties that bind the endogenous form of the receptor or to the constitutively activated form of the receptor, and which inhibit the baseline intracellular response initiated by the active form of the receptor below the normal base level of activity which is observed in the absence of agonists or partial agonists, or decrease GTP binding to membranes. Preferably, the baseline intracellular response is inhibited in the presence of the inverse agonist by at least 30%, more preferably by at least 50%, and most preferably by at least 75%, as compared with the baseline response in the absence of the inverse agonist.

LIGAND shall mean an endogenous, naturally occurring molecule specific for an endogenous, naturally occurring receptor.

PHARMACEUTICAL COMPOSITION shall mean a composition comprising at least one active ingredient, whereby the composition is amenable to investigation for a specified, efficacious outcome in a mammal (for example, and not limitation, a human). Those of ordinary skill in the art will understand and appreciate the techniques appropriate for determining whether an active ingredient has a desired efficacious outcome based upon the needs of the artisan.

STIMULATE or **STIMULATING**, in relationship to the term “response” shall mean that a response is increased in the presence of a compound as opposed to in the absence of the compound.

DETAILED DESCRIPTION

I. Particularly preferred mutations

For convenience, the sequence information regarding the non-endogenous, constitutively active human 5-HT_{2A} and 5-HT_{2C} receptors are referred to by identifiers as set forth in Table 2:

TABLE 2

IDENTIFIER	RECEPTOR	SEQ.ID.NO:	FIGURE
AP-1 cDNA	5-HT _{2C}	28	5a
AP-1	5-HT _{2C}	29	5b
AP-3 cDNA	5-HT _{2A}	30	6a
AP-3	5-HT _{2A}	31	6b
AP-4 cDNA	5-HT _{2A}	32	7a
AP-4	5-HT _{2A}	33	7b

- 5 As will be discussed in greater detail below, a mutation analogous to that reported by Casey (C322K) was utilized in the human 5-HT_{2A} receptor and is referred to herein as AP-2. However, AP-2 did not lead to sufficient constitutive activation to allow for utilization in screening techniques.

II. Introduction

- 10 While it is sometimes possible to make predictions as to the effect of nucleic acid manipulation from one species to another, this is not always the case. The results reported by Casey suggest that a point mutation in the rat 5-HT_{2A} receptor evidences constitutive activation of the mutated receptor. Casey reports that the C322K mutation was approximately four fold more active than the native rat 5-HT_{2A} receptor. However, for purposes of a most preferred use, i.e., screening of candidate compounds, this corresponding mutation in the
- 15 human 5-HT_{2A} receptor had little discernable effect in evidencing constitutive activation of the human receptor. This, of course, creates the reasonable conclusion that the information reported in Herrick-Davis 1 or Herrick-Davis 2 is of limited predictive value relative to the manipulation of the human 5-HT_{2C} receptor. Consequently, the ability to make reasonable
- 20 predictions about the effects of mutations to the rat 5-HT receptors vis-à-vis the corresponding human receptors is not possible. Nonetheless, this unfortunate lack of reasonable predictability

provides the opportunity for others to discover mutations to the human 5-HT receptors that provide evidence of constitutive activation.

Therefore, the present invention is based upon the desire of defining mutated sequences of the human serotonin receptors 5-HT2A and 5-HT2C whereby such mutated versions of the expressed receptor are constitutively active. These constitutively active receptors allow for, inter alia, screening candidate compounds.

What has been discovered and disclosed herein is that substantial activation of the human 5-HT2A receptor can be obtained by "domain swapping," i.e., by switching the third intracellular domain of the 5-HT2A receptor with the third intracellular domain of the 5-HT2C receptor. Additionally, swapping the cytoplasmic tail of the two receptors further increases the IP3 response. Furthermore, mutation of the serine at position 310 to lysine (S310K) of the human 5-HT2C receptor leads to constitutive activation.

What follows is a most preferred approach to identification of candidate compounds; those in the art will readily appreciate that the particular order of screening approaches, and/or whether or not to utilize certain of these approaches, is a matter of choice. Thus, the order presented below, set for presentational efficiency and for indication of the most preferred approach utilized in screening candidate compounds, is not intended, nor is to be construed, as a limitation on the disclosure, or any claims to follow.

III. Generic G Protein-Coupled Receptor screening assay techniques

When a G protein receptor becomes constitutively active, it binds to a G protein (Gq, Gs, Gi, Go) and stimulates the binding of GTP to the G protein. The G protein then acts as a GTPase and slowly hydrolyzes the GTP to GDP, whereby the receptor, under normal conditions, becomes deactivated. However, constitutively activated receptors continue to exchange GDP to GTP. A non-hydrolyzable analog of GTP, [³⁵S]GTPγS, can be used to monitor enhanced binding to membranes which express constitutively activated receptors. It is reported that [³⁵S]GTPγS can be used to monitor G protein coupling to membranes in the absence and presence of ligand. An example of this monitoring, among other examples well-known and available to those in the art, was reported by Traynor and Nahorski in 1995. The preferred use of this assay system is for initial screening of candidate compounds because the system is generically applicable to all G protein-coupled receptors regardless of the particular G protein that interacts with the intracellular domain of the receptor.

IV. Confirmation of G Protein-Coupled Receptor site screening assay techniques

Once candidate compounds are identified using the “generic” G protein-coupled receptor assay (i.e. an assay to select compounds that are agonists, partial agonists, or inverse agonists), further screening to confirm that the compounds have interacted at the receptor site is preferred. For example, a compound identified by the “generic” assay may not bind to the receptor, but may instead merely “uncouple” the G protein from the intracellular domain. Thus, by further screening those candidate compounds, which have been identified using a “generic” assay in an agonist and/or antagonist competitive binding assay, further refinement in the selection process is provided.

Lysergic acid diethylamide (LSD) is a well-known agonist of the 5-HT_{2A} and 5-HT_{2C} receptors, while mesulergine is a well-known antagonist to the 5-HT_{2C} receptor. Accordingly, in most preferred embodiments, an agonist (LSD) and/or antagonist (mesulergine) competitive binding assay(s) is used to further screen those compounds selected from the “generic” assay for confirmation of serotonin receptor binding.

V. Specified G Protein assay techniques

The art-accepted physiologically mediated pathway for the human 5-HT_{2A} and 5-HT_{2C} receptors is via G_q. Intracellular accumulation of IP₃ can be used to confirm constitutive activation of these types of G_q coupled receptors (*see* Herrick-Davis-1). As a result, “IP₃ accumulation” assays can be used to further screen those compounds selected from an agonist and/or antagonist competitive binding assay.

VI. Pharmaceutical compositions

Candidate compounds selected for further development can be formulated into pharmaceutical compositions using techniques well known to those in the art. Suitable pharmaceutically-acceptable carriers are available to those in the art; for example, see Remington’s Pharmaceutical Sciences, 16th Edition, 1980, Mack Publishing Co., (Oslo et al., eds.)

EXAMPLES

The following examples are presented for purposes of elucidation, and not limitation, of the present invention. While specific nucleic acid and amino acid sequences are disclosed herein, those of ordinary skill in the art are credited with the ability to make minor modifications to these sequences while achieving the same or substantially similar results reported below. It is intended that equivalent, non-endogenous, constitutively

activated human serotonin receptor sequences having eighty-five percent (85%) homology, more preferably having ninety percent (90%) homology, and most preferably having ninety-five percent (95%) homology to the disclosed and claimed sequences all fall within the scope of any claims appended hereto.

Example 1

GENERATION OF NON-ENDOGENOUS, CONSTITUTIVELY ACTIVATED HUMAN SEROTONIN RECEPTORS 5-HT_{2C} AND 5-HT_{2A}

A. Construction of constitutively active 5-HT_{2C} receptor cDNA

1. *Endogenous Human 5-HT_{2C}*

The cDNA encoding endogenous human 5-HT_{2C} receptor was obtained from human brain poly-A⁺ RNA by RT-PCR. The 5' and 3' primers were derived from the 5' and 3' untranslated regions and contained the following sequences:

5'-GACCTCGAGGTTGCTTAAGACTGAAGCA-3' (SEQ.ID.NO:1)

5'-ATTTCTAGACATATGTAGCTTGTACCGT-3' (SEQ.ID.NO:2)

PCR was performed using either TaqPlusTM precision polymerase (Stratagene) or rTthTM polymerase (Perkin Elmer) with the buffer systems provided by the manufacturers, 0.25 μM of each primer, and 0.2 mM of each of the four (4) nucleotides. The cycle condition was 30 cycles of 94°C for 1 minute, 57 °C for 1 minute and 72 °C for 2 minutes. The 1.5 kb PCR fragment was digested with Xho I and Xba I and subcloned into the Sal I-Xba I site of pBluescript.

The derived cDNA clones were fully sequenced and found to correspond to published sequences.

2. *AP-1 cDNA*

The cDNA containing a S310K mutation (AP-1 cDNA) in the third intracellular loop of the human 5-HT_{2C} receptor was constructed by replacing the Sty I restriction fragment containing amino acid 310 with synthetic double stranded oligonucleotides encoding the
5 desired mutation. The sense strand sequence utilized had the following sequence:

5'-

CTAGGGGCACCATGCAGGCTATCAACAATGAAAGAAAAGCTAAGAAAGTC-3'
(SEQ. ID.NO: 3)

and the antisense strand sequence utilized had the following sequence:

10 5'-CAAGGACTTTCTTAGCTTTTCTTTCATTGTTGATAGCCTGCATGGT
GCCC-3' (SEQ. ID. NO: 4).

B. Construction of constitutively active 5-HT_{2A} receptor cDNA

1. *Endogenous Human 5-HT_{2A}*

The cDNA encoding endogenous human 5-HT_{2A} receptor was obtained by RT-PCR
15 using human brain poly-A⁺ RNA; a 5' primer from the 5' untranslated region with a Xho I restriction site:

5'-GACCTCGAGTCCTTCTACACCTCATC-3' (SEQ.ID.NO:5)

and a 3' primer from the 3' untranslated region containing an Xba I site:

5'-TGCTCTAGATTCCAGATAGGTGAAAA CTTG-3' (SEQ.ID.NO:6).

20 PCR was performed using either TaqPlus™ precision polymerase (Stratagene) or rTth™ polymerase (Perkin Elmer) with the buffer systems provided by the manufacturers, 0.25 μM of each primer, and 0.2 mM of each of the four (4) nucleotides. The cycle condition was 30 cycles of 94°C for 1 minute, 57 °C for 1 minute and 72 °C for 2 minutes. The 1.5 kb PCR fragment was digested with Xba I and subcloned into the Eco RV-Xba I site of pBluescript.

25 The resulting cDNA clones were fully sequenced and found to encode two amino acid changes from the published sequences. The first change is a T25N mutation in the N-terminal extracellular domain and the second change is an H452Y mutation. These mutations are likely to represent sequence polymorphisms rather than PCR errors since the cDNA clones having the same two mutations were derived from two independent PCR
30 procedures using Taq polymerase from two different commercial sources (TaqPlus™ Stratagene and rTth™ Perkin Elmer).

2. *Human 5-HT_{2A} (C322K; AP-2)*

The cDNA containing the point mutation C322K in the third intracellular loop was constructed by using the Sph I restriction enzyme site, which encompasses amino acid 322. For the PCR procedure, a primer containing the C322K mutation:

5'-CAAAGAAAGTACTGGGCATCGTCTTCTTCCT-3' (SEQ.ID.NO:7)

- 5 was used along with the primer from the 3' untranslated region set forth above as SEQ.ID.NO:6. The resulting PCR fragment was then used to replace the 3' end of the wild type 5-HT2A cDNA by the T4 polymerase blunted Sph I site. PCR was performed using pfu polymerase (Stratagene) with the buffer system provided by the manufacturer and 10% DMSO, 0.25 mM of each primer, 0.5mM of each of the 4 nucleotides. The cycle conditions
- 10 were 25 cycles of 94°C for 1 minute, 60°C for 1 minute and 72°C for 1 minute.

3. *AP-3 cDNA*

The human 5-HT2A cDNA with intracellular loop 3 (IC3) or IC3 and cytoplasmic tail replaced by the corresponding human 5-HT2C cDNA was constructed using PCR-based mutagenesis.

(a) *Replacement of IC3 Loop*

The IC3 loop of human 5-HT2A cDNA was first replaced with the corresponding human 5-HT2C cDNA. Two separate PCR procedures were performed to generate the two fragments, Fragment A and Fragment B, that fuse the 5-HT2C IC3 loop to the transmembrane 6 (TM6) of 5-HT2A. The 237 bp PCR fragment, Fragment A, containing 5-HT2C IC3 and the initial 13 bp of 5-HT2A TM6 was amplified by using the following primers:

5'-CCGCTCGAGTACTGCGCCGACAAGCTTTGAT-3' (SEQ.ID.NO:8)

5'-CGATGCCCAGCACTTTCGAAGCTTTTCTTTCATTGTTG3'(SEQ.ID.NO:9)

The template used was human 5-HT2C cDNA.

The 529 bp PCR fragment, Fragment B, containing the C-terminal 13 bp of IC3 from 5-HT2C and the C-terminal of 5-HT2A starting at beginning of TM6, was amplified by using the following primers:

5'-AAAAGCTTCGAAAGTGCTGGGCATCGTCTTCTTCCT-3' (SEQ.ID.NO:10)

5'-TGCTCTAGATTCCAGATAGGTGAAAAGTTG-3' (SEQ.ID.NO: 11)

The template used was human 5-HT2A cDNA.

Second round PCR was performed using Fragment A and Fragment B as co-templates with SEQ.ID.NO:8 and SEQ.ID.NO:11 (it is noted that the sequences for SEQ.ID.NOS.: 6 and 11 are the same) as primers. The resulting 740 bp PCR fragment, Fragment C, contained the IC3 loop of human 5-HT2C fused to TM6 through the end of the cytoplasmic tail of human 5-HT2A. PCR was performed using pfuTM polymerase (Stratagene) with the buffer system provided by the manufacturer, and 10% DMSO, 0.25 mM of each primer, and 0.5 mM of each of the four (4) nucleotides. The cycle conditions were 25 cycles of 94 °C for 1 minute, 57 °C (1st round PCR) or 60 °C (2nd round PCR) for 1 minute, and 72 °C for 1 minute (1st round PCR) or 90 seconds. (2nd round PCR).

To generate a PCR fragment containing a fusion junction between the human 5-HT2A TM5 and the IC3 loop of 5-HT2C, four (4) primers were used. The two external primers, derived from human 5-HT2A, had the following sequences:

5'-CGTGTCTCTCCTTACTTCA-3' (SEQ.ID.NO:12)

The other primer used was SEQ.ID.NO.6 (see note above regarding SEQ.ID.NOS. 6 and 11). The first internal primer utilized was an antisense strand containing the initial 13 bp of IC3 of 5-HT2C followed by the terminal 23 bp derived from TM5 of 5-HT2A:

5'-TCGGCGCAGTACTTTGATAGTTAGAAAGTAGGTGAT-3' (SEQ.ID.NO:13)

5 The second internal primer was a sense strand containing the terminal 14 bp derived from TM5 of 5-HT2A followed by the initial 24 bp derived from IC3 of 5-HT2C:

5'-TTCTAACTATCAAAGTACTGCGCCGACAAGCTTTGATG-3'

(SEQ.ID.NO:14).

PCR was performed using endogenous human 5-HT2A and a co-template, Fragment C, in a 50 ml reaction volume containing 1X pfu buffer, 10% DMSO, 0.5 mM of each of the four (4) nucleotides, 0.25 mM of each external primer (SEQ.ID.NOS. 11 and 12), 0.06 mM of each internal primer (SEQ.ID.NOS. 13 and 14) and 1.9 units of pfu polymerase (Stratagene). The cycle conditions were 25 cycles of 94°C for 1 minute, 52°C for 1 minute and 72 °C for 2 minutes and 10 seconds. The 1.3 kb PCR product was then gel purified and digested with Pst I and Eco RI. The resulting 1 kb PstI-Eco RI fragment was used to replace the corresponding fragment in the endogenous human 5-HT2A sequence to generate the mutant 5-HT2A sequence encoding the IC3 loop of 5-HT2C.

(b) Replacement of the cytoplasmic tail

To replace the cytoplasmic tail of 5-HT2A with that of 5-HT2C, PCR was performed using a sense primer containing the C-terminal 22 bp of TM7 of endogenous human 5-HT2A followed by the initial 21 bp of the cytoplasmic tail of endogenous human 5-HT2C:

5'-TTCAGCAGTCAACCCACTAGTCTATACTCTGTTCAACAAAATT-3'

(SEQ.ID.NO:15)

25 The antisense primer was derived from the 3' untranslated region of endogenous human 5-HT2C:

5'-ATTTCTAGACATATGTAGCTTGTACCGT-3' (SEQ.ID.NO:16).

The resulting PCR fragment, Fragment D, contained the last 22 bp of endogenous human 5-HT2A TM7 fused to the cytoplasmic tail of endogenous human 5-HT2C. Second round PCR was performed using Fragment D and the co-template was endogenous human 5-HT2A that was previously digested with Acc I to avoid undesired amplification. The antisense primer used was SEQ.ID.NO:16 (the sequences for SEQ.ID.NOS. 16 and 2 are the same) and the sense primer used was derived from endogenous human 5-HT2A:

5'-ATCACCTACTTTCTAACTA-3' (SEQ.ID.NO:17).

PCR conditions were as set forth in Example 1B3.(a) for the first round PCR, except that the annealing temperature was 48 °C and the extension time was 90 seconds. The resulting 710 bp PCR product was digested with Apa I and Xba I and used to replace the
5 corresponding Apa I-Xba I fragment of either (a) endogenous human 5-HT2A, or (b) 5-HT2A with 2C IC3 to generate (a) endogenous human 5-HT2A with endogenous human 5-HT2C cytoplasmic tail and (b) AP-3, respectively.

4. *AP-4 cDNA*

10 This mutant was created by replacement of the region of endogenous human 5-HT2A from amino acid 247, the middle of TM5 right after Pro²⁴⁶, to amino acid 337, the middle of TM6 just before Pro³³⁸, by the corresponding region of AP-1 cDNA. For convenience, the junction in TM5 is referred to as the "2A-2C junction," and the junction in TM6 is referred to as the "2C-2A junction."

15 Three PCR fragments containing the desired hybrid junctions were generated. The 5' fragment of 561 bp containing the 2A-2C junction in TM5 was generated by PCR using endogenous human 5-HT2A as template, SEQ.ID.NO:12 as the sense primer, and the antisense primer was derived from 13 bp of 5-HT2C followed by 20 bp of 5-HT2A sequence:

20 5'-CCATAATCGTCAGGGGAATGAAAAATGACACAA-3' (SEQ.ID.NO:18)

The middle fragment of the 323 bp contains endogenous human 5-HT2C sequence derived from the middle of TM5 to the middle of TM6, flanked by 13 bp of 5-HT2A sequences from the 2A-2C junction and the 2C-2A junction. This middle fragment was generated by using AP-1 cDNA as a template, a sense primer containing 13 bp of 5-HT2A
25 followed by 20 bp of 5-HT2C sequences across the 2A-2C junction and having the sequence:

5'-ATTTTTCATTCCCCTGACGATTATGGTGATTAC-3' (SEQ.ID.NO:19);

and an antisense primer containing 13 bp of 5-HT2A followed by 20 bp of 5-HT2C sequences across the 2C-2A junction and having the sequence:

30 5'-TGATGAAGAAAGGGCACCACATGATCAGAAACA-3' (SEQ.ID.NO:20).

The 3' fragment of 487 bp containing the 2C-2A junction was generated by PCR using endogenous human 5-HT2A as a template and a sense primer having the following sequence from the 2C-2A junction:

5'-GATCATGTGGTGCCCTTTCTTCATCACAAACAT-3' (SEQ.ID.NO:21)

and the antisense primer was SEQ.ID.NO:6 see note above regarding SEQ.ID.NOS. 6 and 11).

Two second round PCR reactions were performed separately to link the 5' and middle fragment (5'M PCR) and the middle and 3' fragment (M3' PCR). The 5'M PCR co-
5 template used was the 5' and middle PCR fragment as described above, the sense primer was SEQ.ID.NO:12 and the antisense primer was SEQ.ID.NO:20. The 5'M PCR procedure resulted in an 857 bp PCR fragment.

The M3' PCR used the middle and M3' PCR fragment described above as the co-
10 template, SEQ.ID.NO: 19 as the sense primer and SEQ.ID.NO:6 (see note above regarding SEQ.ID.NOS. 6 and 11) as the antisense primer, and generated a 784 bp amplification product. The final round of PCR was performed using the 857 bp and 784 bp fragments from the second round PCR as the co-template, and SEQ.ID.NO:12 and SEQ.ID.NO: 6 (see
15 note above regarding SEQ.ID.NOS. 6 and 11) as the sense and the antisense primer, respectively. The 1.32 kb amplification product from the final round of PCR was digested with Pst I and Eco RI. Then resulting 1 kb Pst I-Eco RI fragment was used to replace the corresponding fragment of the endogenous human 5-HT2A to generate mutant 5-HT2A with 5-HT2C: C310K/IC3. The Apa I-Xba fragment of AP3 was used to replace the
20 corresponding fragment in mutant 5-HT2A with 5-HT2C: C310K/IC3 to generate AP4.

Example 2

RECEPTOR EXPRESSION

A. pCMV

Although a variety of expression vectors are available to those in the art, for
25 purposes of utilization for both the endogenous and non-endogenous receptors discussed herein, it is most preferred that the vector utilized be pCMV. This vector was deposited with the American Type Culture Collection (ATCC) on October 13, 1998 (10801 University Blvd., Manassas, VA 20110-2209 USA) under the provisions of the Budapest Treaty for the International Recognition of the Deposit of Microorganisms for the Purpose of Patent
30 Procedure. The DNA was tested by the ATCC and determined to be viable. The ATCC has assigned the following deposit number to pCMV: ATCC #203351. See Figure 8.

B. Transfection procedure

For the generic assay ($[^{35}\text{S}]\text{GTP}\gamma\text{S}$; Example 3) and the antagonist binding assay (mesulergine; Example 4), transfection of COS-7 or 293T cells was accomplished using the following protocol.

On day one, 5×10^6 COS-7 cells or 1×10^7 293T cells per 150mm plate were plated out.
5 On day two, two reaction tubes were prepared (the proportions to follow for each tube are per plate): tube A was prepared by mixing 20 μg DNA (e.g., pCMV vector; pCMV vector AP-1 cDNA, etc.) in 1.2ml serum free DMEM (Irvine Scientific, Irvine, CA); tube B was prepared by mixing 120 μl lipofectamine (Gibco BRL) in 1.2ml serum free DMEM. Tubes A and B were then admixed by inversions (several times), followed by incubation at room temperature
10 for 30-45min. The admixture is referred to as the "transfection mixture". Plated COS-7 cells were washed with 1X PBS, followed by addition of 10ml serum free DMEM. 2.4ml of the transfection mixture was then added to the cells, followed by incubation for 4hrs at 37°C/5% CO_2 . The transfection mixture was then removed by aspiration, followed by the addition of 25ml of DMEM/10% Fetal Bovine Serum. Cells were then incubated at 37°C/5% CO_2 . After
15 72hr incubation, cells were then harvested and utilized for analysis.

Example 3

GTP MEMBRANE BINDING SCINTILLATION PROXIMITY ASSAY

20 The advantages of using $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ binding to measure constitutive activation are that: (a) $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ binding is generically applicable to all G protein-coupled receptors; and (b) $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ binding is proximal at the membrane surface, thereby making it less likely to pick-up molecules which affect the intracellular cascade. The assay utilizes the ability of G protein-coupled receptors to stimulate $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ binding to membranes expressing the
25 relevant receptors. Therefore, the assay may be used to directly screen compounds at the disclosed serotonin receptors.

Figure 9 demonstrates the utility of a scintillation proximity assay to monitor the binding of $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ to membranes expressing the endogenous human 5-HT_{2C} receptor expressed in COS cells. In brief, the assay was incubated in 20 mM HEPES, pH 7.4, binding
30 buffer with 0.3 nM $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ and 12.5 μg membrane protein and 1 μM GDP for 30 minutes. Wheatgerm agglutinin beads (25 μl ; Amersham) were then added and the mixture was incubated for another 30 minutes at room temperature. The tubes were then centrifuged at 1500

x g for 5 minutes at room temperature and then counted in a scintillation counter. As shown in Figure 9, serotonin, which as the endogenous ligand activates the 5-HT_{2C} receptor, stimulated [³⁵S]GTPγS binding to the membranes in a concentration dependant manner. The stimulated binding was completely inhibited by 30 μM mianserin, a compound considered as a classical 5-HT_{2C} antagonist, but also known as a 5-HT_{2C} inverse agonist.

Although this assay measures agonist-induced binding of [³⁵S]GTPγS to membranes and can be routinely used to measure constitutive activity of receptors, the present cost of wheatgerm agglutinin beads may be prohibitive. A less costly but equally applicable alternative also meets the needs of large-scale screening. Flash plates and WallacTM scintistrips may be used to format a high throughput [³⁵S]GTPγS binding assay. This technique allows one to monitor the tritiated ligand binding to the receptor while simultaneously monitoring the efficacy via [³⁵S]GTPγS binding. This is possible because the WallacTM beta counter can switch energy windows to analyze both tritium and ³⁵S-labeled probes.

Also, this assay may be used for detecting of other types of membrane activation events that result in receptor activation. For example, the assay may be used to monitor ³²P phosphorylation of a variety of receptors (including G protein-coupled and tyrosine kinase receptors). When the membranes are centrifuged to the bottom of the well, the bound [³⁵S]GTPγS or the ³²P-phosphorylated receptor will activate the scintillant coated on the wells. Use of Scinti[®] strips (WallacTM) demonstrate this principle. Additionally, this assay may be used for measuring ligand binding to receptors using radiolabeled ligands. In a similar manner, the radiolabeled bound ligand is centrifuged to the bottom of the well and activates the scintillant. The [³⁵S]GTPγS assay results parallel the results obtained in traditional second messenger assays of receptors.

As shown in Figure 10, serotonin stimulates the binding of [³⁵S]GTPγS to the endogenous human 5-HT_{2C} receptor, while mianserin inhibits this response. Furthermore, mianserin acts as a partial inverse agonist by inhibiting the basal constitutive binding of [³⁵S]GTPγS to membranes expressing the endogenous human 5-HT_{2C} receptor. As expected, there is no agonist response in the absence of GDP since there is no GDP present to exchange for [³⁵S]GTPγS. Not only does this assay system demonstrate the response of the native 5-HT_{2C} receptor, but it also measures the constitutive activation of other receptors.

Figure 11A and Figure 11B demonstrate the enhanced binding of [³⁵S]GTPγS to membranes prepared from 293T cells expressing the control vector alone, the native human 5-HT_{2C} receptor or the AP-1 receptor. The total protein concentration used in the assay affects the total amount of [³⁵S]GTPγS binding for each receptor. The c.p.m. differential between the CMV transfected and the constitutively active mutant receptor increased from approximately 1000 c.p.m at 10 μg/well to approximately 6-8000 c.p.m. at 75 μg/well protein concentration, as shown in Figure 11.

The AP-1 receptor showed the highest level of constitutive activation followed by the wild type receptor, which also showed enhanced [³⁵S]GTPγS binding above basal. This is consistent with the ability of the endogenous human 5-HT_{2C} receptor to accumulate intracellular IP₃ in the absence of 5HT stimulation (Example 5) and is also consistent with published data claiming that the endogenous human 5-HT_{2C} receptor has a high natural basal activity. Therefore, the AP-1 receptor demonstrates that constitutive activity may be measured by proximal [³⁵S]GTPγS binding events at the membrane interface.

Example 4

SEROTONIN RECEPTOR AGONIST/ANTAGONIST COMPETITIVE BINDING ASSAY

Membranes were prepared from transfected COS-7 cells (*see* Example 2) by homogenization in 20 mM HEPES and 10 mM EDTA, pH 7.4 and centrifuged at 49,000 x g for 15 min. The pellet was resuspended in 20 mM HEPES and 0.1 mM EDTA, pH 7.4, homogenized for 10 sec. using polytron homogenizer (Brinkman) at 5000 rpm and centrifuged at 49,000 x g for 15 min. The final pellet was resuspended in 20 mM HEPES and 10 mM MgCl₂, pH 7.4, homogenized for 10 sec. using polytron homogenizer (Brinkman) at 5000 rpm.

Assays were performed in triplicate 200μl volumes in 96 well plates. Assay buffer (20 mM HEPES and 10 mM MgCl₂, pH 7.4) was used to dilute membranes, ³H-LSD, ³H-mesulergine, serotonin (used to define non-specific for LSD binding) and mianserin (used to define non-specific for mesulergine binding). Final assay concentrations consisted of 1nM ³H-LSD or 1nM ³H-mesulergine, 50μg membrane protein and 100μM serotonin or mianserin. LSD assays were incubated for 1 hr at 37° C, while mesulergine assays were incubated for 1 hr at room temperature. Assays were terminated by rapid filtration onto Wallac Filtermat Type B with ice cold binding buffer using Skatron cell harvester. The radioactivity was determined in a Wallac 1205 BetaPlate counter.

Example 5**INTRACELLULAR IP3 ACCUMULATION ASSAY**

5 For the IP3 accumulation assay, a transfection protocol different from the protocol set forth in Example 2 was utilized. In the following example, the protocols used for days 1-3 were slightly different for the data generated for Figures 12 and 14 and for Figures 13 and 15; the protocol for day 4 was the same for all conditions.

A. COS-7 and 293 Cells

10 On day one, COS-7 cells or 293 cells were plated onto 24 well plates, usually 1×10^5 cells/well or 2×10^5 cells/well, respectively. On day two, the cells were transfected by first mixing 0.25 μ g DNA (*see* Example 2) in 50 μ l serum-free DMEM/well and then 2 μ l lipofectamine in 50 μ l serum-free DMEM/well. The solutions ("transfection media") were gently mixed and incubated for 15-30 minutes at room temperature. The cells were washed
15 with 0.5 ml PBS and then 400 μ l of serum free media was mixed with the transfection media and added to the cells. The cells were then incubated for 3-4 hours at 37°C/5%CO₂. Then the transfection media was removed and replaced with 1ml/well of regular growth media. On day 3, the media was removed and the cells were washed with 0.5 ml PBS. Then 0.5 ml inositol-free/serum-free media (GIBCO BRL) was added to each well with 0.25 μ Ci
20 of ³H-myo-inositol/well and the cells were incubated for 16-18 hours overnight at 37°C/5%CO₂. Protocol A.

B. 293 Cells

On day one, 1×10^7 293 cells per 150mm plate were plated out. On day two, two reaction tubes were prepared (the proportions to follow for each tube are per plate): tube A was
25 prepared by mixing 20 μ g DNA (e.g., pCMV vector; pCMV vector AP-1 cDNA, etc.) in 1.2ml serum free DMEM (Irvine Scientific, Irvine, CA); tube B was prepared by mixing 120 μ l lipofectamine (Gibco BRL) in 1.2ml serum free DMEM. Tubes A and B were then admixed by inversions (several times), followed by incubation at room temperature for 30-45min. The admixture is referred to as the "transfection mixture". Plated 293 cells were washed with
30 1XPBS, followed by addition of 10ml serum free DMEM. 2.4ml of the transfection mixture was then added to the cells, followed by incubation for 4hrs at 37°C/5% CO₂. On day 3, cells were trypsinized and counted, followed by plating of 1×10^6 cells/well (poly D-lysine treated

12-well plates). Cells were permitted to adhere to the wells, followed by one wash with 1xPBS. Thereafter, 0.5 μ Ci 3 H-inositol in 1ml inositol-free DMEM was added per well. Protocol B.

On day 4, the cells were washed with 0.5 ml PBS and then 0.45 ml of assay medium was added containing inositol-free/serum free media, 10 μ M pargyline, 10 mM lithium chloride, or 0.4 ml of assay medium and 50 μ l of 10x ketanserin (ket) to a final concentration of 10 μ M. The cells were then incubated for 30 minutes at 37°C. Then the cells were washed with 0.5 ml PBS and 200 μ l of fresh/icecold stop solution (1M KOH; 18 mM Na-borate; 3.8 mM EDTA) was added/well. The solution was kept on ice for 5-10 minutes or until the cells were lysed and then neutralized by 200 μ l of fresh/ice cold neutralization sol. (7.5 % HCL). The lysate was then transferred into 1.5 ml micro-centrifuge tubes and 1 ml of chloroform/methanol (1:2) was added/tube. The solution was vortexed for 15 seconds and the upper phase was applied to a Biorad AG1-X8 anion exchange resin (100-200 mesh). The resin was washed with water and 0.9 ml of the upper phase was loaded onto the column. The column was washed with 10 mls of 5 mM myo-inositol and 10 ml of 5 mM Na-borate/60mM Na-formate. The inositol trisphosphates were eluted into scintillation vials containing 10 ml of scintillation cocktail with 2 ml of 0.1 M formic acid/ 1 M ammonium formate. The columns were regenerated by washing with 10 ml of 0.1 M formic acid/3M ammonium formate and rinsed twice with dd H₂O and stored at room temperature in water. Results are discussed below.

Figure 12 is an illustration of IP₃ production from the human 5-HT_{2A} receptor which was mutated using the same point mutation as set forth in Casey, which rendered the rat receptor constitutively active. The results represented in Figure 12, support the position that when the point mutation shown to activate the rat receptor is introduced into the human receptor, little activation of the receptor is obtained that would allow for appropriate screening of candidate compounds, with the response being only moderately above that of the endogenous human 5-HT_{2A} receptor. Generally, a response of at least 2X above that of the endogenous response is preferred.

Figure 13 provides an illustration comparing IP₃ production from endogenous 5-HT_{2A} receptor and the AP4 mutation. The results illustrated in Figure 13 support the position that when the novel mutation disclosed herein is utilized, a robust response of constitutive IP₃ accumulation is obtained (e.g., over 2X that of the endogenous receptor).

Figure 14 provides an illustration of IP3 production from AP3. The results illustrated in Figure 14 support the position that when the novel mutation disclosed herein is utilized, a robust response of constitutive IP3 accumulation is obtained.

Figure 15 provides bar-graph comparisons of IP3 accumulation between endogenous human 5-HT2C receptor and AP-1. Note that the endogenous receptor has a high degree of natural constitutive activity relative to the control CMV transfected cells (i.e., the endogenous receptor appears to be constitutively activated).

Example 6

SCREENING OF COMPOUNDS KNOWN TO HAVE 5-HT2C ANTAGONIST ACTIVITY AGAINST NON-ENDOGENOUS, CONSTITUTIVELY ACTIVATED HUMAN SEROTONIN RECEPTOR: AP-1

A final concentration of 12.5 μ g membranes prepared from COS7 cells (see Example 2) transiently expressing constitutively active mutant human 5HT2C receptor AP-1 were incubated with binding buffer (20 mM HEPES, pH 7.4, 100 mM NaCl, 20 mM MgCl₂·6H₂O, 0.2% saponin, and 0.2 mM ascorbate), GDP(1 μ M) and compound in a 96-well plate format for a period of 60 minutes at ambient room temperature. Plates were then centrifuged at 4,000 rpm for 15 minutes followed by aspiration of the reaction mixture and counting for 1 minute in a Wallac™ MicroBeta plate scintillation counter. A series of compounds known to possess reported 5HT2C antagonist activity were determined to be active in the [³⁵S]GTP γ S binding assay using AP-1. IC₅₀ determinations were made for these commercially available compounds (RBI, Natick, MA). Results are summarized in Table 3. For each determination, eight concentrations of test compounds were tested in triplicate. The negative control in these experiments consisted of AP-1 receptor without test compound addition, and the positive control consisted of 12.5 μ g/well of COS7 cell membranes expressing the CMV promoter without expressed AP-1 receptor.

TABLE 3

Test Compound	Known Pharmacology	IC ₅₀ (nM) in GTP- γ -[³⁵ S] Assay
Metergoline	5HT2/1C antagonist	32.0

Mesulergine	5HT2/1C antagonist	21.2
Methysergide	5HT2/1C antagonist	6.1
Methiothepin	5HT1 antagonist	20.4
Normethylclozapin	5HT2/1C antagonist	21.4
Fluoxetine	5HT reuptake inhibitor	114.0
Ritanserin	5HT2/1C antagonist	19.4

The IC₅₀ results confirm that the seven tested compounds showed antagonist activity at the AP-1 receptor.

Example 7

5 SCREENING OF CANDIDATE COMPOUNDS AGAINST NON-ENDOGENOUS, CONSTITUTIVELY ACTIVATED HUMAN SEROTONIN RECEPTORS:AP-1

Approximately 5,500 candidate compounds (Tripos, Inc., St. Louis, MO) were screened using the assay protocol of Example 3 (with AP-1 mutant receptor) for identification as inverse agonists against the receptor; for this assay, an arbitrary cut-off of at least 50% inhibition was established for identification of inverse agonists. Approximately 120 of these compounds evidenced at least 50% inhibition of [³⁵S]GTPγS binding at 10 μM candidate compound (data not shown).

Example 8

15 SCREENING OF SELECTED COMPOUNDS TO CONFIRM RECEPTOR BINDING: AP-1

The candidate compounds identified from Example 7 were then screened using the assay protocol of Example 4 (mesulergine), using the AP-1 mutant receptor. IC₅₀ (nM) values were determined; five of the nearly 120 compounds of Example 7 were determined to have potent binding affinity for the receptor. Results are summarized in Table 4.

Table 4

Candidate Compound	IC ₅₀ (nM) in Mesulergine Assay
102461	205.0
102788	46.5
100341	209.0
100431	147.0
103487	1,810.0

Example 9a

GENERAL SCREENING PARADIGM:

SELECTION OF PRE-CLINICAL CANDIDATE LEADS

The "primary" screen designed to directly identify human 5HT_{2A}/5HT_{2C} receptor inverse agonists consisted of a membrane-based GTP γ S binding assay utilizing membranes prepared from COS7 cells transiently transfected with AP-1 human receptor. Candidate compounds (10 μ M final assay concentration) directly identified as inhibiting receptor-mediated increases in GTP γ S binding by greater than 50-75% (arbitrary cut-off value) were considered active "hits". Primary assay hits were then re-tested in the same assay to reconfirm their inverse agonist activity. If primary assay hits were reconfirmed active (50% or greater inhibition), and therefore directly identified as, *e.g.*, an inverse agonist, one of two approaches were available: (a) so-called "directed libraries" could be created, *i.e.*, additional candidate compounds were synthesized based upon the structures of the reconfirmed hits (geared towards, *e.g.*, improvement in the characteristics of the compounds) whereby the directed library compounds were then evaluated for the ability to compete for radioligand binding to both mutant 5HT_{2C} (AP-1) and endogenous 5HT_{2A} receptors, or (b) the reconfirmed hits were then evaluated for the ability to compete for radioligand binding to both mutant 5HT_{2C} (AP-1) and endogenous 5HT_{2A} receptors. Thus, when approach (a) was used, because these directed library candidate compounds were based upon the structures of compounds that were directly identified from the

membrane-based GTP γ S binding assay, the directed library compounds were not re-tested in the membrane-based GTP γ S binding assay but rather were then confirmed via the radioligand binding analysis. The radioligand binding analysis tests were initially performed at 10 μ M test compound in triplicate and if the compound inhibited radiolabeled binding by 50% or more, the analysis was followed by eight concentration competition curves to determine K_i values. The last step in secondary assay evaluation was to determine if test compounds were capable of inhibiting AP-3 receptor-mediated accumulation of inositol phosphates (e.g., IP₃). This final assay confirms that the directly identified compounds retained inverse agonist properties.

Example 9b

CONSTITUTIVELY ACTIVATED HUMAN 5HT_{2C} RECEPTOR (AP-1) MEDIATED FACILITATION OF GTP γ S BINDING TO COS7 MEMBRANES

This protocol is substantially the same as set forth above in Example 6.

Primary screening assays measuring GTP γ S binding to membranes prepared from COS7 cells transiently transfected with human mutated 5HT_{2C} receptor (AP-1) were used to directly identify inverse agonists in screening libraries (Tripos, Inc.). Candidate compound screens were performed in a total assay volume of 200 μ l using scintillant-coated Wallac ScintistripTM plates. The primary assay was comprised of the following chemicals (at indicated final assay concentrations): 20 mM HEPES, pH 7.4, 100 mM NaCl, 20 mM MgCl₂, 0.2% saponin, 0.2 mM ascorbic acid, 1 μ M GDP, 0.3 nM GTP γ ³⁵S, and 12.5 μ g of the above defined membranes. Incubations were performed for 60 minutes at ambient room temperature. The binding assay incubation was terminated by centrifugation of assay plates at 4,000 rpm for 15 minutes, followed by rapid aspiration of the reaction mixture and counting in a Wallac MicroBetaTM scintillation counter.

Primary screening of candidate compounds initially involved testing of 72 test compounds per assay plate (96-well plates were utilized), at a final assay concentration of 10 μ M candidate compound, in single replicates. A total of sixteen wells of each plate were dedicated for an eight concentration clozapine (a confirmed 5HT_{2C}/2A inverse agonist) dose response curve (duplicate determinations at each concentration). Finally, a total of five assay wells of each plate were dedicated to define the negative control (AP-1 receptor

expressing membranes without addition of candidate compounds) and three wells from each plate to define the positive control (membranes without AP-1 receptor).

Reconfirmation experiments involve re-testing candidate compounds in the same assay described above, except that candidate compounds were evaluated in triplicate, thus
5 allowing evaluation of 24 compounds per 96-well assay plate. Similar to the primary assay plates, an eight concentration clozapine dose response curve (duplicate determinations at each concentration) and the same negative and positive control wells were also included within each 96-well plate.

Example 9c(1)

COMPETITION STUDIES

MUTATED HUMAN 5HT_{2C} RECEPTOR (AP-1)

15 Radioligand binding competition experiments were performed in a total assay volume of 200µl using standard 96-well microtiter plates. The final assay ingredients consisted of assay buffer (20mM HEPES and 10mM MgCl₂), 1nM [³H]mesulergine, and 50µg of membranes (COS7 with AP-1 as defined above). Nonspecific [³H]mesulergine binding was defined in the presence of 100µM mianserin. Incubations were performed for 1 hour at 37°C.
20 Receptor bound radioligand was resolved from free radioligand by rapid filtration of the assay mixture over a Wallac Filtermat™ Type B filter, followed by washing with ice-cold assay buffer using a Skatron™ cell harvester. Radioactivity was counted using a Wallac 1205 BetaPlate™ counter. Each assay plate contained five negative control wells (membranes expressing receptor and no candidate compound addition) and three positive control wells
25 (each containing 100µM mianserin). For one concentration tests, candidate compounds were diluted into assay buffer and screened at a final concentration of 10µM, in triplicate. For IC₅₀ determinations, candidate compounds were diluted in assay buffer and eight different concentrations were evaluated, in triplicate. A total of 16 wells were designated for an eight concentration mianserin dose response curve evaluation for both assays.

Example 9c(2)

COMPETITION STUDIES

WILD TYPE HUMAN 5HT2A RECEPTOR

Radioligand binding competition experiments were performed in a total assay volume of 200µl using standard 96-well microtiter plates. The final assay ingredients comprised assay buffer (20mM HEPES and 10mM MgCl₂), 1nM [³H]LSD, and 50µg of the above-defined membranes (COS7 with AP-1). Nonspecific [³H]LSD binding was defined in the presence of 100µM serotonin. Incubations were performed for 1 hour at 37°C. Receptor bound radioligand was resolved from free radioligand by rapid filtration of the assay mixture over a Wallac Filtermat™ Type B filter, followed by washing with ice-cold assay buffer using a Skatron™ cell harvester. Radioactivity was counted using a Wallac 1205 BetaPlate™ counter. Each assay plate contained five negative control wells (membranes expressing receptor and no candidate compound addition) and three positive control wells (containing 100µM mianserin). For one concentration tests, candidate compounds were diluted into assay buffer and screened at a final concentration of 10µM in triplicate. For IC₅₀ determinations, candidate compounds were diluted in assay buffer and eight different concentrations were evaluated in triplicate. A total of 16 wells were designated for an eight concentration serotonin dose response curve evaluation for both assays.

Example 9d

RECEPTOR-MEDIATED INOSITOL PHOSPHATE ACCUMULATION

Candidate compound identified in the assays of Examples 9a-9c were then evaluated for inositol phosphate accumulation, following the protocol of Example 5 (COS7 cells expressing human mutated 5HT2A receptor, AP-3), modified as follows: tube A was prepared by mixing 16 µg DNA (e.g., pCMV vector; pCMV vector AP-1 cDNA, etc.) in 1.0ml serum free DMEM (Irvine Scientific, Irvine, CA); tube B was prepared by mixing 60µl lipofectamine (Gibco BRL) in 1.0 ml serum free DMEM. Tubes A and B were then admixed by inversions (several times), followed by incubation at room temperature for 30 min. The admixture is referred to as the "transfection mixture". Plated 293 cells were washed with 10 ml Serum Free DMEM, followed by addition of 11 ml Serum Free DMEM. 2.0 ml of the transfection mixture was then added to the cells, followed by incubation for 5hrs at 37°C/5% CO₂. On day 3, cells were trypsinized and counted, followed by plating of 1x10⁶ cells/well

(12-well plates). Cells were permitted to adhere to the wells for 8 hrs., followed by one wash with 1x PBS. Thereafter, 0.5 μ Ci 3 H-inositol in 1 ml inositol-free DMEM was added per well.

On day 4, the cells were washed with 1.5 ml PBS and then 0.9 ml of assay medium was added containing inositol-free/serum free media, 10 μ M pargyline, 10 mM lithium chloride, for 5 min in 37°C/5% CO₂ followed by 100 μ l addition of candidate compound diluted in the same material. The cells were then incubated for 120 minutes at 37°C. Then the cells were washed with 1.5 ml PBS and 200 μ l of fresh/icecold stop solution (1M KOH; 18 mM Na-borate; 3.8 mM EDTA) was added/well. The solution was kept on ice for 5-10 minutes or until the cells were lysed and then neutralized by 200 μ l of fresh/ice cold neutralization sol. (7.5 % HCL). The lysate was then transferred into 1.5 ml micro-centrifuge tubes and 1 ml of chloroform/methanol (1:2) was added/tube. The solution was vortexed for 15 seconds and the upper phase was applied to a Biorad AG1-X8 anion exchange resin (100-200 mesh). The resin was washed with water and 0.9 ml of the upper phase was loaded onto the column. The column was washed with 10 mls of 5 mM myo-inositol and 10 ml of 5 mM Na-borate/60mM Na-formate. The inositol trisphosphates were eluted into scintillation vials containing 10 ml of scintillation cocktail with 2 ml of 0.1 M formic acid/ 1 M ammonium formate. The columns were regenerated by washing with 10 ml of 0.1 M formic acid/3M ammonium formate and rinsed twice with dd H₂O and stored at room temperature in water.

Following this round of assaying, candidate compounds having an IC₅₀ value of less than 10 μ M were considered as potential leads for the development of pharmaceutical compositions.

SCREENING CANDIDATE COMPOUNDS

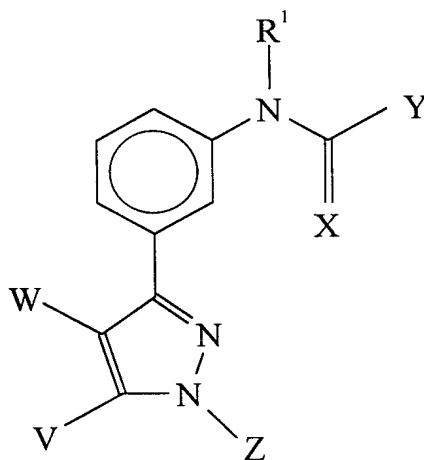
Following the protocols set forth above, one compound, 103487 (Example 8, *supra*) evidenced the following results:

Figure Number	GTP γ S AP-1 Percent Inhibition Relative	GTP γ S AP-1 Percent Inhibition Relative To	Competitive Binding AP-1 ([3 H]mesulergine)	Competitive Binding WT 5HT2A ([3 H]LSD)	Inositol Phosphate Accumulation AP-3

	To Positive Control (Primary)	Positive Control (Reconfirm)	IC ₅₀ Value (nM)	IC ₅₀ Value (nM)	IC ₅₀ Value (nM)
15A (103487)	-1%	31%	2100 850	46	52 90

Based upon these results, structure activity analysis of the 103487 compound suggested that a series of derivatives of 3-(4-bromo-1-methylpyrazole-3-yl)phenylamine would exhibit similar 5-HT_{2A} activity and selectivity. A series of derivatives of 3-(4-bromo-1-methylpyrazole-3-yl)phenylamine have now been synthesized. These “directed” library compounds (Tripos, Inc.) were then analyzed in accordance with the protocols of Examples 9c(1), 9c(2) and 9d.

This series of compounds exhibits highly selective 5-HT_{2A} activity. Accordingly, in the first aspect of the invention, a series of compounds possessing 5-HT_{2A} receptor activity that are useful as inverse agonists at such receptors is designated by the general formula (A):



(A)

Wherein:

W is lower alkyl (C₁₋₆), or halogen;

V is lower alkyl (C₁₋₆), or halogen;

X is either Oxygen or Sulfur;

Y is NR^2R^3 , or $(\text{CH}_2)_m\text{R}^4$, or $\text{O}(\text{CH}_2)_n\text{R}^4$;

Z is lower alkyl (C_{1-6});

$m = 0 - 4$

$n = 0 - 4$

R^1 is H or lower alkyl (C_{1-4});

R^2 is H or lower alkyl (C_{1-4});

R^3 and R^4 are independently a C_{1-6} alkyl, or C_{2-6} alkenyl, or cycloalkyl, or aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from CF_3 , CCl_3 , Me, NO_2 , OH, OMe, OEt, CONR^5R^6 , NR^5R^6 , OCF_3 , SMe, COOR^7 , $\text{SO}_2\text{NR}^5\text{R}^6$, SO_3R^7 , COMe, COEt, CO-lower alkyl, SCF_3CN , C_{2-6} alkenyl, H, halogens, C_{1-4} alkoxy, C_{3-6} cycloalkyl, C_{1-6} alkyl, aryl, and aryloxy wherein each of the C_{3-6} cycloalkyl, C_{1-6} alkyl, aryl, or aryloxy groups may be further optionally substituted by up to four substituents in any position independently selected from CF_3 , CCl_3 , Me, NO_2 , OH, OMe, OEt, CONR^5R^6 , NR^5R^6 , NHCOCH_3 , OCF_3 , SMe, COOR^7 , SO_3R^7 , $\text{SO}_2\text{NR}^5\text{R}^6$, COMe, COEt, CO-lower alkyl, SCF_3 , CN, C_{2-6} alkenyl, H, halogens, C_{1-4} alkoxy, C_{3-6} cycloalkyl, C_{1-6} alkyl, and aryl;

R^5 and R^6 are independently a H, or C_{1-6} alkyl, or C_{2-6} alkenyl, or cycloalkyl, or aryl, or CH_2 aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from CF_3 , CCl_3 , Me, NO_2 , OH, OMe, OEt, CONR^7R^8 , NR^7R^8 , NHCOCH_3 , OCF_3 , SMe, COOR^9 , SO_3R^7 , $\text{SO}_2\text{NR}^7\text{R}^8$, COMe, COEt, CO-lower alkyl, SCF_3 , CN, C_{2-6} alkenyl, H, halogens, C_{1-4} alkoxy, C_{3-6} cycloalkyl, C_{1-6} alkyl, and aryl wherein each of the C_{3-6} cycloalkyl, C_{1-6} alkyl, or aryl groups may be further optionally substituted by up to four substituents in any position independently selected from CF_3 , CCl_3 , Me, NO_2 , OH, OMe, OEt, CONR^8R^9 , NR^8R^9 , NHCOCH_3 , OCF_3 , SMe, COOR^7 , $\text{SO}_2\text{NR}^8\text{R}^9$, SO_3R^7 , COMe, COEt, CO-lower alkyl, SCF_3 , CN, C_{2-6} alkenyl, H, halogens, C_{1-4} alkoxy, C_{3-6} cycloalkyl, C_{1-6} alkyl, and aryl,

or R^5 and R^6 may form part of a 5, 6 or 7 membered cyclic structure which may be either saturated or unsaturated and that may contain up to four heteroatoms selected from O, N or S and said cyclic structure may be optionally substituted by up to four substituents in any position independently selected from CF_3 , CCl_3 , Me,

NO₂, OH, OMe, OEt, OCF₃, SMe, COOR⁷, SO₂NR⁸R⁹, SO₃R⁷, NHCOCH₃, COEt, COMe, or halogen;

R⁷ may be independently selected from H or C₁₋₆ alkyl;

R⁸ and R⁹ are independently a H, or C₁₋₆ alkyl, or C₂₋₆ alkenyl, or cycloalkyl, or aryl, or CH₂aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from halogen, CF₃, OCF₃, OEt, CCl₃, Me, NO₂, OH, OMe, SMe, COMe, CN, COOR⁷, SO₃R⁷, COEt, NHCOCH₃, or aryl;

an aryl moiety can be a 5 or 6 membered aromatic heterocyclic ring (containing up to 4 hetero atoms independently selected from N, O, or S) or a 6 membered aromatic non-heterocyclic ring or a polycycle;

C₁₋₆ alkyl moieties can be straight chain or branched;

optionally substituted C₁₋₆ alkyl moieties can be straight chain or branched;

C₂₋₆ alkenyl moieties can be straight chain or branched; and

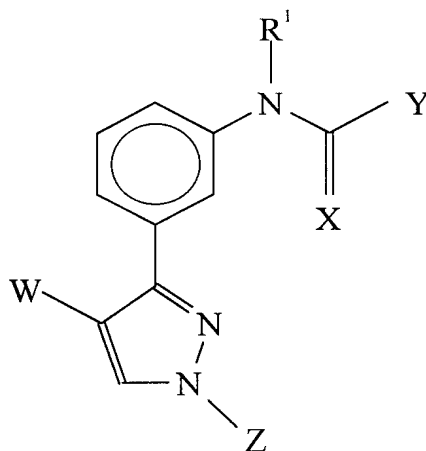
optionally substituted C₂₋₆ alkenyl moieties can be straight chain or branched.

Examples of suitable C₁₋₆ alkyl groups include but are not limited to methyl, ethyl, n-propyl, i-propyl, n-butyl, and t-butyl.

Halogens are typically F, Cl, Br, and I.

Examples of 5 or 6 membered ring moieties include, but are not restricted to, phenyl, furanyl, thienyl, imidazolyl, pyridyl, pyrrolyl, oxazolyl, isoxazolyl, triazolyl, pyrazolyl, tetrazolyl, thiazolyl and isothiazolyl. Examples of polycycle moieties include, but are not restricted to, naphthyl, benzothiazolyl, benzofuranyl, benzimidazolyl, quinolyl, isoquinolyl, indolyl, quinoxalinyl, quinazolinyl and benzothienyl.

A more preferred series of compounds possessing 5-HT_{2A} receptor activity that are useful as inverse agonists at such receptors is designated by the general formula (B):



(B)

Wherein:

W is Me, or Et, or halogen;

X is either Oxygen or Sulfur;

5 Y is NR^2R^3 , or $(\text{CH}_2)_m\text{R}^4$, or $\text{O}(\text{CH}_2)_n\text{R}^4$;

Z is lower alkyl (C_{1-6});

$m = 0 - 4$

$n = 0 - 4$

R^1 is H or lower alkyl (C_{1-4});

10 R^2 is H or lower alkyl (C_{1-4});

R^3 and R^4 are independently a C_{1-6} alkyl, or C_{2-6} alkenyl, or cycloalkyl, or aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from CF_3 , CCl_3 , Me, NO_2 , OH, OMe, OEt, CONR^5R^6 , NR^5R^6 , OCF_3 , SMe, COOR^7 , $\text{SO}_2\text{NR}^5\text{R}^6$, SO_3R^7 , COMe, COEt, CO-lower alkyl, SCF_3CN , C_{2-6} alkenyl, H, halogens, C_{1-4} alkoxy, C_{3-6} cycloalkyl, C_{1-6} alkyl, aryl, and aryloxy wherein each of the C_{3-6} cycloalkyl, C_{1-6} alkyl, aryl, or aryloxy groups may be further optionally substituted by up to four substituents in any position independently selected from CF_3 , CCl_3 , Me, NO_2 , OH, OMe, OEt, CONR^5R^6 , NR^5R^6 , NHCOCH_3 , OCF_3 , SMe, COOR^7 , SO_3R^7 , $\text{SO}_2\text{NR}^5\text{R}^6$, COMe, COEt, CO-lower alkyl, SCF_3 , CN, C_{2-6} alkenyl, H, halogens, C_{1-4} alkoxy, C_{3-6} cycloalkyl, C_{1-6} alkyl, and aryl;

15

20

R^5 and R^6 are independently a H, or C_{1-6} alkyl, or C_{2-6} alkenyl, or cycloalkyl, or aryl, or CH_2 aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from CF_3 , CCl_3 , Me, NO_2 , OH, OMe, OEt, $CONR^7R^8$, NR^7R^8 , $NHCOCH_3$, OCF_3 , SMe, $COOR^9$, SO_3R^7 , $SO_2NR^7R^8$, COMe, COEt, CO-lower alkyl, SCF_3 , CN, C_{2-6} alkenyl, H, halogens, C_{1-4} alkoxy, C_{3-6} cycloalkyl, C_{1-6} alkyl, and aryl wherein each of the C_{3-6} cycloalkyl, C_{1-6} alkyl, or aryl groups may be further optionally substituted by up to four substituents in any position independently selected from CF_3 , CCl_3 , Me, NO_2 , OH, OMe, OEt, $CONR^8R^9$, NR^8R^9 , $NHCOCH_3$, OCF_3 , SMe, $COOR^7$, $SO_2NR^8R^9$, SO_3R^7 , COMe, COEt, CO-lower alkyl, SCF_3 , CN, C_{2-6} alkenyl, H, halogens, C_{1-4} alkoxy, C_{3-6} cycloalkyl, C_{1-6} alkyl, and aryl,

or R^5 and R^6 may form part of a 5, 6 or 7 membered cyclic structure which may be either saturated or unsaturated and that may contain up to four heteroatoms selected from O, N or S and said cyclic structure may be optionally substituted by up to four substituents in any position independently selected from CF_3 , CCl_3 , Me, NO_2 , OH, OMe, OEt, OCF_3 , SMe, $COOR^7$, $SO_2NR^8R^9$, SO_3R^7 , $NHCOCH_3$, COEt, COMe, or halogen;

R^7 may be independently selected from H or C_{1-6} alkyl;

R^8 and R^9 are independently a H, or C_{1-6} alkyl, or C_{2-6} alkenyl, or cycloalkyl, or aryl, or CH_2 aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from halogen, CF_3 , OCF_3 , OEt, CCl_3 , Me, NO_2 , OH, OMe, SMe, COMe, CN, $COOR^7$, SO_3R^7 , COEt, $NHCOCH_3$, or aryl;

an aryl moiety can be a 5 or 6 membered aromatic heterocyclic ring (containing up to 4 hetero atoms independently selected from N, O, or S) or a 6 membered aromatic non-heterocyclic ring or a polycycle;

C_{1-6} alkyl moieties can be straight chain or branched;

optionally substituted C_{1-6} alkyl moieties can be straight chain or branched;

C_{2-6} alkenyl moieties can be straight chain or branched; and

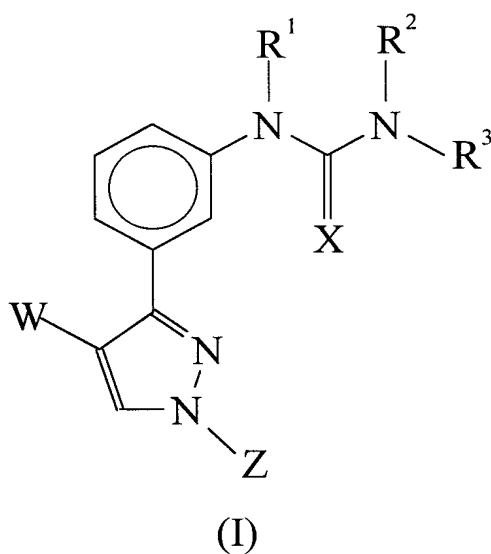
optionally substituted C_{2-6} alkenyl moieties can be straight chain or branched.

Examples of suitable C_{1-6} alkyl groups include but are not limited to methyl, ethyl, n-propyl, i-propyl, n-butyl, and t-butyl.

Halogens are typically F, Cl, Br, and I.

Examples of 5 or 6 membered ring moieties include, but are not restricted to, phenyl, furanyl, thienyl, imidazolyl, pyridyl, pyrrolyl, oxazolyl, isoxazolyl, triazolyl, pyrazolyl, tetrazolyl, thiazolyl and isothiazolyl. Examples of polycycle moieties include, but are not restricted to, naphthyl, benzothiazolyl, benzofuranyl, benzimidazolyl, quinolyl, isoquinolyl, indolyl, quinoxalinyl, quinazolinyl and benzothienyl.

A first series of compounds having 5-HT_{2A} receptor activity is represented by a class (I) of compounds of formula (B) wherein Y=NR²R³:



Wherein:

Preferably R¹ and R² are H.

Preferably W is Br.

Preferably X is O.

Preferably Z is Me.

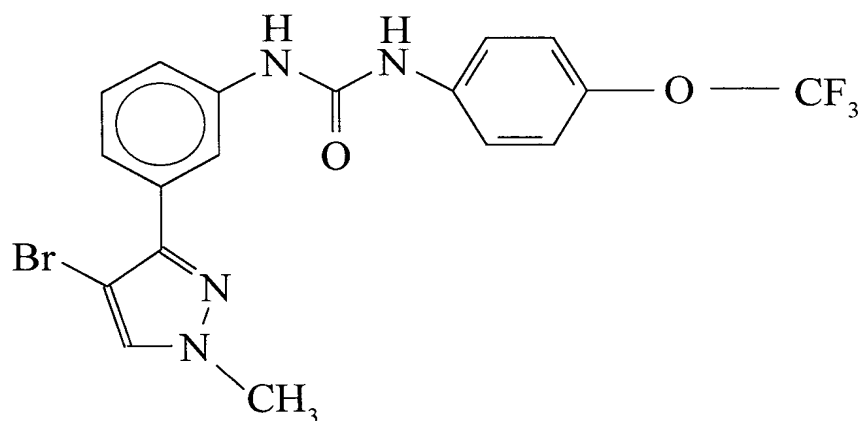
Preferably R³ is 4-trifluoromethoxyphenyl or 4-trifluoromethoxybenzyl.

Preferred compounds are:

37

103487

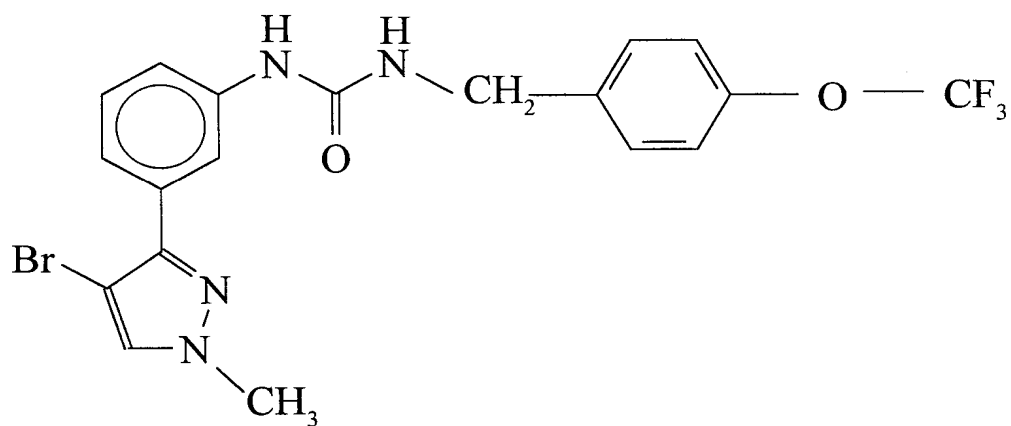
N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][{(4-trifluoromethoxy)phenyl}amino] carboxamide



5

116115

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][{(4-trifluoromethoxy)phenyl)methyl}amino]carboxamide



10

These two compounds demonstrated the following activities using the assay protocols defined in the Examples above:

Compound Number	Competitive Binding AP-1 ([³ H]mesulergine) IC ₅₀ Value (μM)	Competitive Binding WT 5HT _{2A} ([³ H]LSD) IC ₅₀ Value (μM)	Inositol Phosphate Accumulation AP-3 IC ₅₀ Value (μM)
103487	2.1	.046	.052
116115	1.2	.45	.0171

Additional compounds of formula (B) wherein Y=NR²R³ are set forth below.

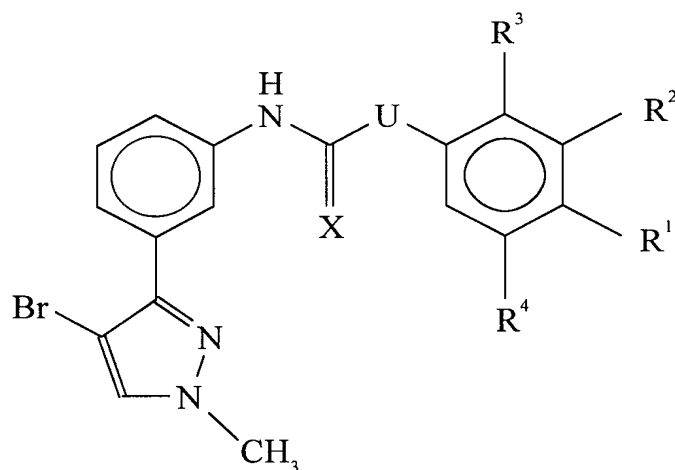
Inositol phosphate accumulation assays evidence the activity of test compounds. Both single concentration percentages of control values and IC₅₀ determinations indicate activity. In the tables below the column legends have the following meanings:

IP₃ % Contol: The values in this column reflect an IP Accumulation Assay where the test compounds were evaluated at one concentration of 10 μM. For these assays, the compound was diluted into inositol-free Dulbecco's Eagle Media containing 10 μM pargyline and 10 mM LiCl and tested at a final assay concentration of 10 μM, in triplicate. The percent control value was calculated based on the control in which no test compound was added.

IP₃ AP-3 IC₅₀ nM: The values in this column reflect an IP accumulation assay in which the test compound was evaluated at several different concentrations whereby an IC₅₀ could be determined. This column corresponds to the column appearing in the tables above which is labeled: Inositol Phosphate Accumulation, AP-3, IC₅₀ Value (μM).

WT 5HT_{2A} LSD IC₅₀ nM: The values in this column reflect a competitive binding assay using LSD. This column corresponds to the column appearing in the tables above which is labeled: Competitive Binding, WT 5HT_{2A}, ([³H]LSD), IC₅₀ Value (μM).

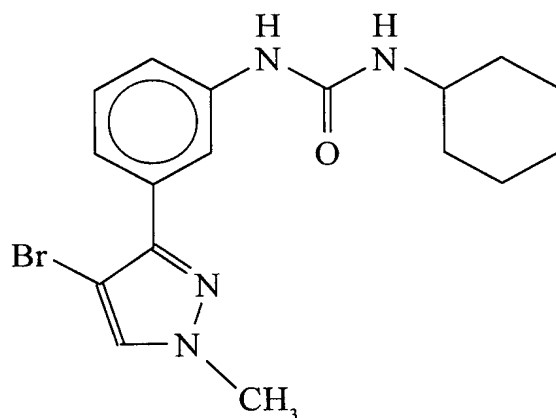
Compounds listed in each of the following tables reference the structures immediately preceding the table. A "dash" in the table indicates that no value was determined.



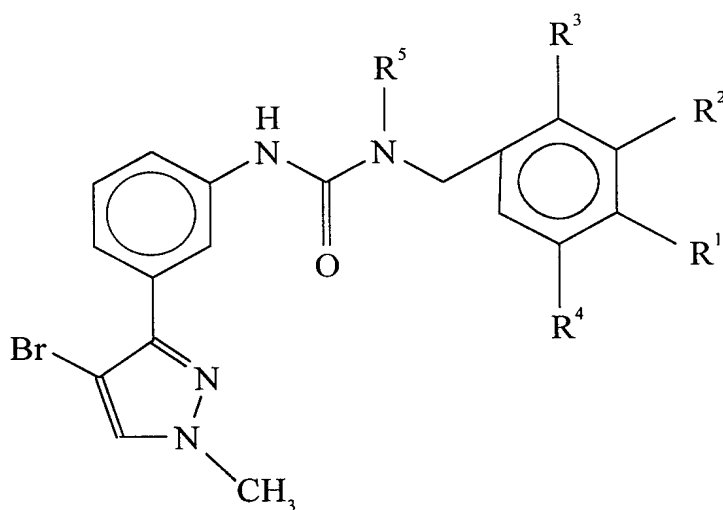
Compound No.	R ¹	R ²	R ³	R ⁴	X	U	IP ₃ % of Control	IP ₃ AP-3 IC ₅₀ nM	WT 5HT _{2A} LSD IC ₅₀ nM
N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][(4-methylthiophenyl)amino]carboxamide									
116079	SCH ₃	H	H	H	O	NH	16	17	4
N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][(4-chlorophenyl)amino]carboxamide									
116081	Cl	H	H	H	O	NH	10	3.2	11
{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(4-fluorophenyl)carboxamide									
116082	F	H	H	H	O	NH	11	-	7
{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-[2-(trifluoromethoxy)phenyl]carboxamide									
116087	H	H	CF ₃ O	H	O	NH	11	-	200
{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(2-nitrophenyl)carboxamide									
116089	H	H	NO ₂	H	O	NH	27	-	238

{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(4-methoxyphenyl)carboxamide									
116091	MeO	H	H	H	O	NH	12	-	19
{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(2-methylphenyl)carboxamide									
116092	H	H	Me	H	O	NH	32	-	131
{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-[4-(trifluoromethyl)phenyl]carboxamide									
116097	CF ₃	H	H	H	O	NH	11	-	65
{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(3-chlorophenyl)carboxamide									
116105	H	Cl	H	H	O	NH	11	-	39
{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(2-chlorophenyl)carboxamide									
116108	H	H	Cl	H	O	NH	6	-	249
{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-[4-(methylethyl)phenyl]carboxamide									
116110	isopropyl	H	H	H	O	NH	7	-	338
{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(3-methoxyphenyl)carboxamide									
116111	H	MeO	H	H	O	NH	7	-	106
{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(3-methylphenyl)carboxamide									
116112	H	Me	H	H	O	NH	14	-	57
[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino-N-methyl-N-[4-(trifluoromethoxy)phenyl]carboxamide									
116113	CF ₃ O	H	H	H	O	NCH ₃	-	193	2
N-[4-(tert-butyl)phenyl]{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}carboxamide									
116119	t-butyl	H	H	H	O	NH	17	-	476
N-[4-(dimethylamino)phenyl]{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}carboxamide									
116122	NMe ₂	H	H	H	O	NH	9	-	309

N-(3,5-dichloro-4-methylphenyl){[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}carboxamide									
116138	Me	Cl	H	Cl	O	NH	23	-	122
{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-[4-(trifluoromethylthio)phenyl]carboxamide									
116139	CF ₃ S	H	H	H	O	NH	12	-	56
{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(2-fluorophenyl)carboxamide									
116144	H	H	F	H	O	NH	12	-	37
2-([3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino)carbonylamino)benzamide									
116145	H	H	CONH ₂	H	O	NH	31	-	7473
{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(4-cyanophenyl)carboxamide									
116147	CN	H	H	H	O	NH	12	-	2
{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(2-cyanophenyl)carboxamide									
116148	H	H	CN	H	O	NH	30	-	348



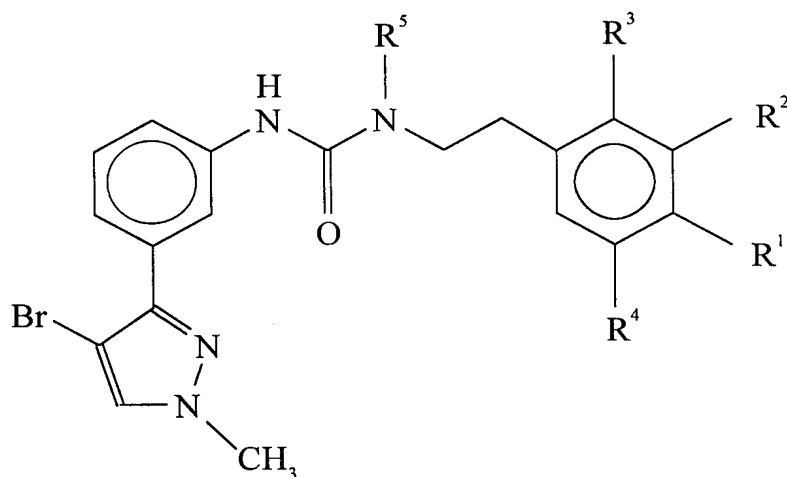
Compound No.	N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][cyclohexylamino]carboxamide	IP ₃ AP-3 IC ₅₀ nM	WT 5HT _{2A} LSD IC ₅₀ nM
116141		114	81



5

Compound No.	R ¹	R ²	R ³	R ⁴	R ⁵	IP ₃ AP-3 IC ₅₀ nM	WT 5HT _{2A} LSD IC ₅₀ nM
N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][phenylmethylamino]carboxamide							
116143	H	H	H	H	H	120	47
N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][{(4-fluorophenyl)methyl} amino]carboxamide							
116182	F	H	H	H	H	89	132

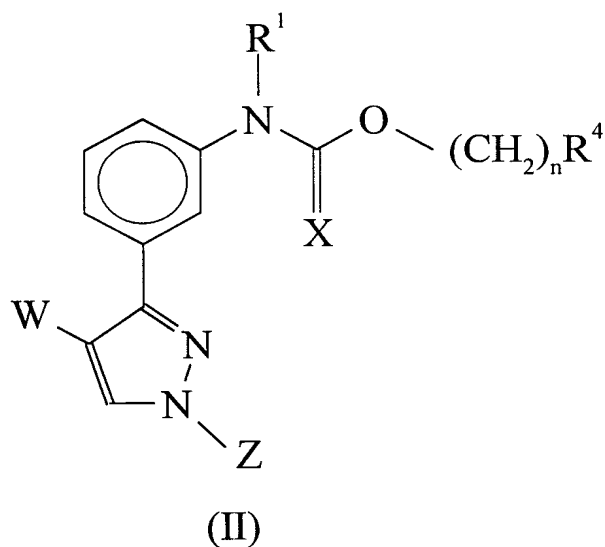
N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][{(3,4-dimethoxyphenyl)methyl}amino]carboxamide							
116183	OMe	OMe	H	H	H	-	1010
N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][{(3,4,5-trimethoxyphenyl)methyl}amino]carboxamide							
116184	OMe	OMe	H	OMe	H	-	2960
N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][{(2-methylphenyl)methyl}amino]carboxamide							
116185	H	H	Me	H	H	-	769
N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][{(4-methoxyphenyl)methyl}amino]carboxamide							
116189	OMe	H	H	H	H	-	102



Compound No.	R ¹	R ²	R ³	R ⁴	R ⁵	IP ₃ AP-3 IC ₅₀ nM	WT 5HT _{2A} LSD IC ₅₀ nM
N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][{2-(4-methoxyphenyl)ethyl} amino]carboxamide							

116194	OMe	H	H	H	H	32	61
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- 5 A second series of compounds having 5-HT_{2A} receptor activity is represented by a class (II) of compounds of formula (B) wherein Y= O(CH₂)_nR⁴:

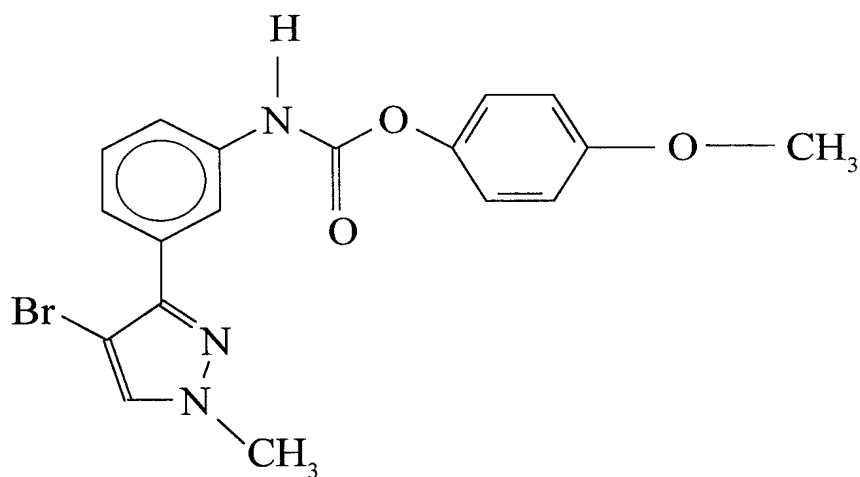


Wherein:

- 10 Preferably R¹ is H.
 Preferably W is Br.
 Preferably X is O.
 Preferably Z is Me.
 Preferably when n = 0, R⁴ is 4-methoxyphenyl or tertiary butyl.
- 15 Preferred compounds are:

116100

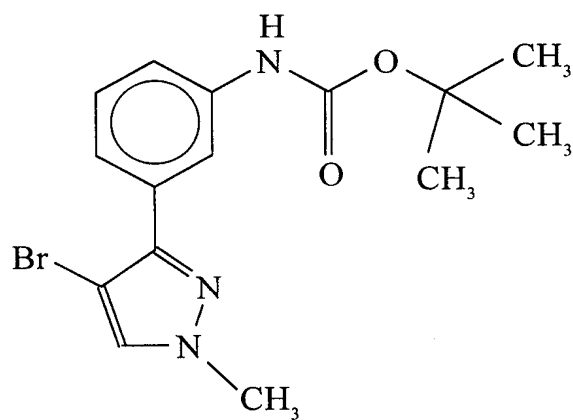
N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][4-methoxyphenoxy]carboxamide



116192

(tert-butoxy)-N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]carboxamide

5



These two compounds demonstrated the following activity:

Compound No.	Competitive Binding AP-1 ([³ H]mesulergine) IC ₅₀ Value (μM)	Competitive Binding WT 5HT _{2A} ([³ H]LSD) IC ₅₀ Value (μM)	Inositol Phosphate Accumulation AP-3 IC ₅₀ Value (μM)
116100	1.8	<0.001	0.0003

116192	-	0.014	0.057
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In addition to the assays discussed above, the specific activity of 116100 at the 5HT_{2A} receptor was further confirmed by the following.

In Vitro Binding of 5HT_{2A} Receptor

5 Animals:

Animals (Sprague-Dawley rats) were sacrificed and brains were rapidly dissected and frozen in isopentane maintained at -42°C. Horizontal sections were prepared on a cryostat and maintained at -20°C.

LSD Displacement Protocol:

10 Lysergic acid diethylamide (LSD) is a potent 5HT_{2A} receptor and dopamine D2 receptor ligand. An indication of the selectivity of compounds for either or both of these receptors involves displacement of radiolabeled-bound LSD from pre-treated brain sections. For these studies, radiolabeled I¹²⁵-LSD (NEN Life Sciences, Boston, MA., Catalogue number NEX-199) was utilized; spiperone (RBI, Natick, MA. Catalogue number s-128), a
15 5HT_{2A} receptor and dopamine D2 receptor antagonist, was also utilized. Buffer consisted of 50 nanomolar TRIS-HCl, pH 7.4

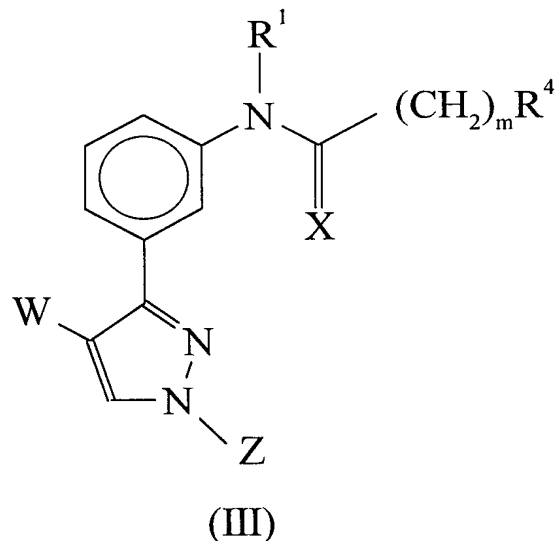
Brain sections were incubated in (a) Buffer plus 1 nanomolar I¹²⁵-LSD; (b) Buffer plus 1 nanomolar I¹²⁵-LSD and 1 micromolar spiperone; or Buffer plus 1 nanomolar I¹²⁵-LSD and 1 micromolar 116100 for 30 minutes at room temperature. Sections were then
20 washed 2X 10 minutes at 4°C in Buffer, followed by 20 seconds in distilled H₂O. Slides were then air-dried.

After drying, sections were apposed to x-ray film (Kodak Hyperfilm) and exposed for 4 days.

Analysis:

25 Figures 16A-C provide representative autoradiographic sections from this study. Figure 16A evidences darker bands (derived from I¹²⁵-LSD binding) primarily in both the fourth layer of the cerebral cortex (primarily 5HT_{2A} receptors), and the caudate nucleus (primarily dopamine D2 receptors and some 5HT_{2A} receptors). As can be seen from Figure 16B, spiperone, which is a 5HT_{2A} and dopamine D2 antagonist, displaces the I¹²⁵-LSD from
30 these receptors on both the cortex and the caudate. As can be further seen from Figure 16C, 116100 appears to selectively displace the I¹²⁵-LSD from the cortex (5HT_{2A}) and not the caudate (dopamine D2).

A third series of compounds having 5-HT_{2A} receptor activity is represented by a class (III) of compounds of formula (B) wherein Y = (CH₂)_mR⁴:



Wherein:

Preferably W is Br.

Preferably X is O.

Preferably Z is Me.

Preferably R¹ is H.

Preferably when m = 0, R⁴ is preferably 4-trifluoromethoxyphenyl, or thiophene, or 4-chlorophenyl.

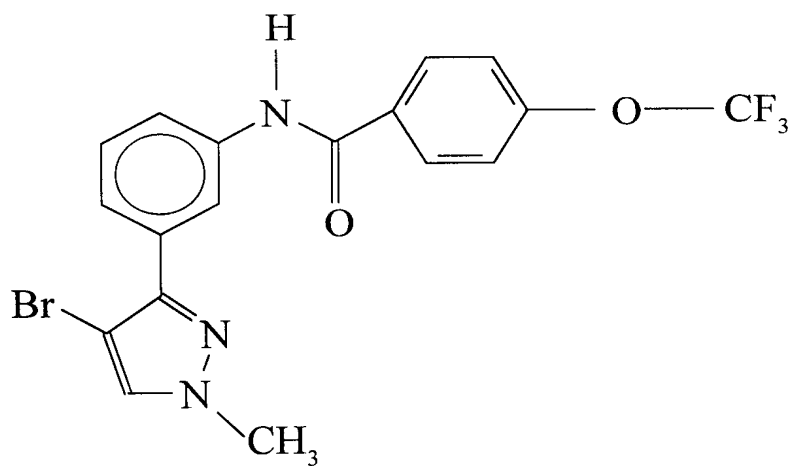
Preferred compounds are:

116101

m = 0, R¹ = H, R⁴ = 4-trifluoromethoxyphenyl

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][4-trifluoromethoxyphenyl]carboxamide

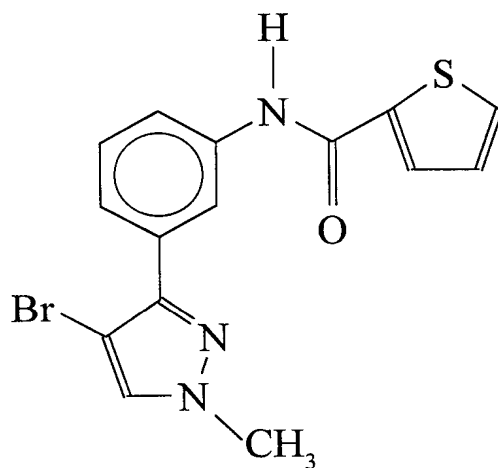
48



116102

$m = 0$, $R^1 = H$, $R^4 = \text{thiophene}$

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][2-thienyl]carboxamide

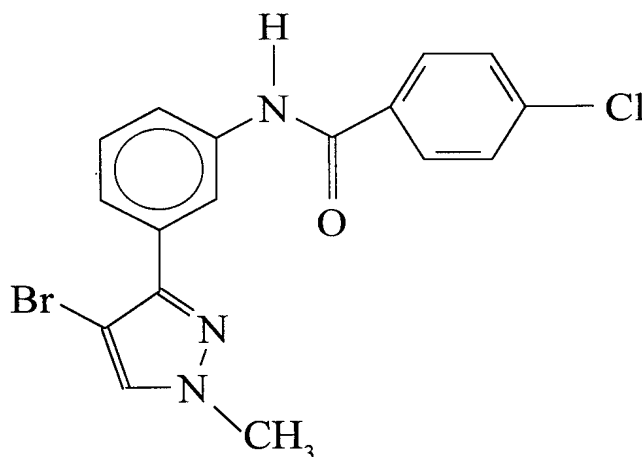


116120

$m = 0$, $R^1 = H$, $R^4 = 4\text{-chlorophenyl}$

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][4-chlorophenyl]carboxamide

10



These three compounds demonstrated the following activities:

Compound Number	Competitive Binding AP-1 ([³ H]mesulergine) IC ₅₀ Value (μM)	Competitive Binding WT 5HT _{2A} ([³ H]LSD) IC ₅₀ Value (μM)	Inositol Phosphate Accumulation AP-3 IC ₅₀ Value (μM)
116101	6.1	.46	0.0213
116102	2.8	.17	0.080
116120	1.2	.21	0.0315

5

In Vivo Analysis of Compound 116102

In addition to the in vitro assays shown in the above table, the in vivo response of animals to the 116102 compound is demonstrated by the following.

A 5HT_{2A} receptor antagonist or inverse agonist is expected to decrease amphetamine-stimulated locomotion without affecting baseline locomotion. *See, for example*, Soresnon, et al, 266(2) J. Pharmacol. Exp. Ther. 684 (1993). Based upon the foregoing information, Compound 116102 is a potent inverse agonist at the human 5HT_{2A} receptor. For the following study, the following parameters and protocol were utilized:

Animals, Vehicle

Adult male Sprague-Dawley rats were utilized for these studies. Animals were housed in groups of 2-3 in hanging plastic cages with food and water available at all times. Animals were weighed and handled for at least one day prior to surgery and throughout the studies. For these studies, Vehicle consisted of 90% ethanol (100%) and 10% water.

15

Amphetamine-stimulated locomotor activity: Assessment and Apparatus

A San Diego Instruments Flex Field apparatus was used to quantify baseline and amphetamine-stimulated locomotor activity. This apparatus consists of four 16" x 16" clear plastic open fields. Photocell arrays (16 in each dimension) interfaced with a personal computer to automatically quantify activity. Several measures of activity can be assessed with the apparatus, including total photocell beam breaks. Animals (vehicle control and Compound treated) were injected s.c. 30 minutes prior to initiation of analysis. Following this 30 minute period, animals were placed individually into an open field and baseline activity was assessed for 30 minutes (habituation phase). Following baseline, animals were removed, injected with d-amphetamine sulfate (1.0 mg/kg) and immediately returned to the open field for 150 minutes, in order to follow the time course (10 minute intervals) of amphetamine-stimulated locomotor activity.

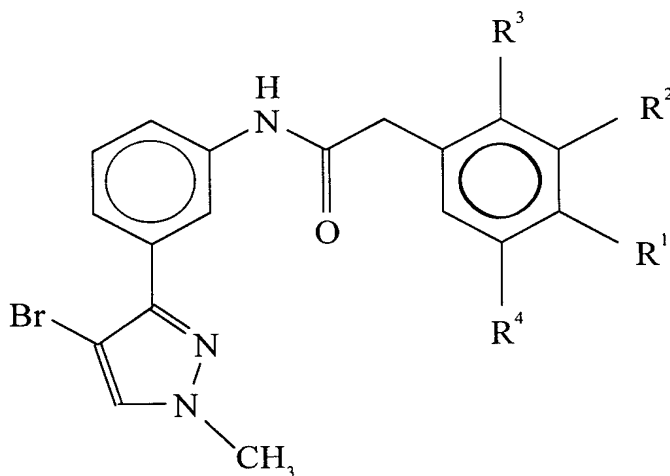
Dosing

Vehicle Control	Compound 116102	Dose (mg/kg)
6 animals	6 animals	0.1
	6 animals	1.0
	6 animals	5.0
	6 animals	10.0

15 Analysis

Results, based upon the number of recorded photobeam breaks (mean +/- sem), are presented in Figure 17A-C. As supported by Figures 17A,B and C, a general "inverted U" shaped pattern was observed (*see, generally, Sahgal, A. "Practical behavioural neuroscience: problems, pitfalls and suggestions" pp 1-8, 5 in Behavioral Neuroscience: A Practical Approach, Volume 1 A. Sahgal (Ed.) 1993, IRL Press, New York*). As Figure 17 also indicates, with exception of the highest dose (10mg/kg), *in vivo*, the tested doses of Compound 116102 evidenced a decrease in the amphetamine-stimulated locomotion, consistent with a 5HT_{2A} receptor antagonist or inverse agonist.

Additional compounds of formula (B) wherein $Y = (CH_2)_m R^4$ are set forth below.

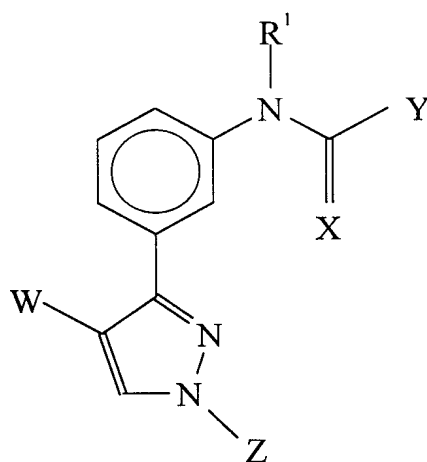


Compound No.	R ¹	R ²	R ³	R ⁴	IP ₃ IC ₅₀ nM	LSD IC ₅₀ nM
N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]-2-[4-(trifluoromethoxy)phenyl]acetamide						
116137	OCF ₃	H	H	H	-	106
N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]-2-(3-fluorophenyl)acetamide						
116174	H	F	H	H	153	318
N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]-2-(3-methoxyphenyl)acetamide						
116175	H	OMe	H	H	108	625
N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]-2-(2-fluorophenyl)acetamide						
116176	H	H	F	H	129	662
N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]-2-(4-nitrophenyl)acetamide						
116177	NO ₂	H	H	H	61	108

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]-2-(2-methoxyphenyl)acetamide						
116178	H	H	OMe	H	165	2300

compound names not provided

Based upon the discovery of the specific inverse agonist activity of the above identified compounds at the 5HT_{2A} receptor, a novel class of compounds has been identified which exhibits said activity. Accordingly, in the second aspect of the invention, there is provided a novel compound of formula (C):



(C)

Wherein:

W is Me, or Et, or halogen;

X is either Oxygen or Sulfur;

Y is NR²R³, or (CH₂)_mR⁴, or O(CH₂)_nR⁴;

Z is lower alkyl (C₁₋₆);

m = 0 - 4;

n = 0 - 4;

R¹ is H or lower alkyl (C₁₋₄);

R² is H or lower alkyl (C₁₋₄);

R³ is a C₁₋₆ alkyl, or C₂₋₆ alkenyl, or cycloalkyl, or (CH₂)_karyl group (k = 1 - 4), preferably k = 1, and each said group may be optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH,

OMe, OEt, CONR⁵R⁶, NR⁵R⁶, OCF₃, SMe, COOR⁷, SO₂NR⁵R⁶, SO₃R⁷, COMe, COEt, CO-lower alkyl, SCF₃CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, aryl, and aryloxy wherein each of the C₃₋₆ cycloalkyl, C₁₋₆ alkyl, aryl, or aryloxy groups may be further optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁵R⁶, NR⁵R⁶, NHCOCH₃, OCF₃, SMe, COOR⁷, SO₃R⁷, SO₂NR⁵R⁶, COMe, COEt, CO-lower alkyl, SCF₃, CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, and aryl;

R⁴ is a C₁₋₆ alkyl, or C₂₋₆ alkenyl, or cycloalkyl, or aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁵R⁶, NR⁵R⁶, OCF₃, SMe, COOR⁷, SO₂NR⁵R⁶, SO₃R⁷, COMe, COEt, CO-lower alkyl, SCF₃CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, aryl, and aryloxy wherein each of the C₃₋₆ cycloalkyl, C₁₋₆ alkyl, aryl, or aryloxy groups may be further optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁵R⁶, NR⁵R⁶, NHCOCH₃, OCF₃, SMe, COOR⁷, SO₃R⁷, SO₂NR⁵R⁶, COMe, COEt, CO-lower alkyl, SCF₃, CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, and aryl;

R⁵ and R⁶ are independently a H, or C₁₋₆ alkyl, or C₂₋₆ alkenyl, or cycloalkyl, or aryl, or CH₂ aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁷R⁸, NR⁷R⁸, NHCOCH₃, OCF₃, SMe, COOR⁹, SO₃R⁷, SO₂NR⁷R⁸, COMe, COEt, CO-lower alkyl, SCF₃, CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, and aryl wherein each of the C₃₋₆ cycloalkyl, C₁₋₆ alkyl, or aryl groups may be further optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁸R⁹, NR⁸R⁹, NHCOCH₃, OCF₃, SMe, COOR⁷, SO₂NR⁸R⁹, SO₃R⁷, COMe, COEt, CO-lower alkyl, SCF₃, CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, and aryl,

or R⁵ and R⁶ may form part of a 5, 6 or 7 membered cyclic structure which may be either saturated or unsaturated and that may contain up to four heteroatoms selected from O, N or S and said cyclic structure may be optionally substituted by up

to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, OCF₃, SMe, COOR⁷, SO₂NR⁸R⁹, SO₃R⁷, NHCOCH₃, COEt, COMe, or halogen;

R⁷ may be independently selected from H or C₁₋₆ alkyl;

5 R⁸ and R⁹ are independently a H, or C₁₋₆ alkyl, or C₂₋₆ alkenyl, or cycloalkyl, or aryl, or CH₂aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from halogen, CF₃, OCF₃, OEt, CCl₃, Me, NO₂, OH, OMe, SMe, COMe, CN, COOR⁷, SO₃R⁷, COEt, NHCOCH₃, or aryl;

10 an aryl moiety can be a 5 or 6 membered aromatic heterocyclic ring (containing up to 4 hetero atoms independently selected from N, O, or S) or a 6 membered aromatic non-heterocyclic ring or a polycycle;

C₁₋₆ alkyl moieties can be straight chain or branched;

optionally substituted C₁₋₆ alkyl moieties can be straight chain or branched;

15 C₂₋₆ alkenyl moieties can be straight chain or branched; and

optionally substituted C₂₋₆ alkenyl moieties can be straight chain or branched;

with the proviso that said compound is not:

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][methylamino]carboxamide, or

20 N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][{(4-trifluoromethoxy)phenyl}amino]carboxamide, or

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][2-chlorophenyl]carboxamide, or

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][2-chloro-3-pyridyl]carboxamide, or

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][trichloromethyl]carboxamide.

25 Examples of suitable C₁₋₆ alkyl groups include but are not limited to methyl, ethyl, n-propyl, i-propyl, n-butyl, and t-butyl.

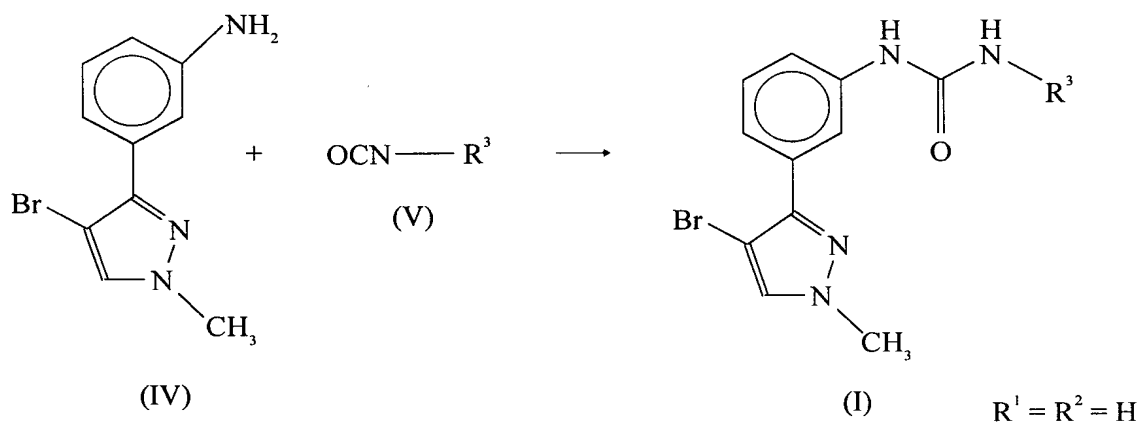
Halogens are typically F, Cl, Br, and I.

30 Examples of 5 or 6 membered ring moieties include, but are not restricted to, phenyl, furanyl, thienyl, imidazolyl, pyridyl, pyrrolyl, oxazolyl, isoxazolyl, triazolyl, pyrazolyl, tetrazolyl, thiazolyl and isothiazolyl. Examples of polycycle moieties include, but are not restricted to, naphthyl, benzothiazolyl, benzofuranyl, benzimidazolyl, quinolyl, isoquinolyl, indolyl, quinoxalyl, quinazolinyl and benzothienyl.

Synthetic Approaches

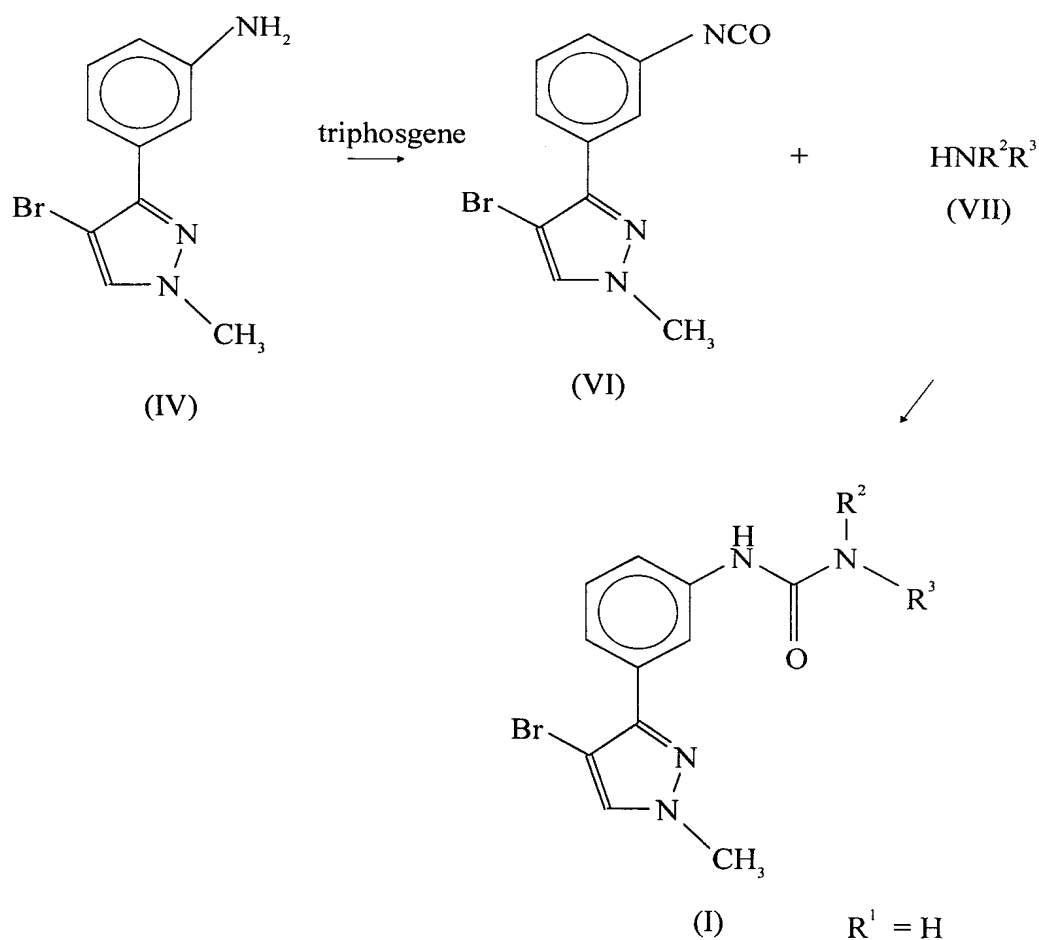
The compounds disclosed in this invention may be readily prepared according to a variety of synthetic manipulations, all of which would be familiar to one skilled in the art. In the general syntheses set forth below, the labeled substituents have the same identifications as set out in the definitions of the compounds above.

Compounds of general formula **(I)** can be obtained *via* a variety of synthetic routes all of which would be familiar to one skilled in the art. The reaction of isocyanates with amines is a commonly practised method for the formation of ureas (see Org. Syn. Coll. Vol. V, (1973), 555). Amine **(IV)**, 3-(4-bromo-1-methylpyrazole-3-yl)phenylamine, commercially available from Maybridge Chemical Company, Catalog No. KM01978, CAS No. 175201-77-1] reacts readily with isocyanates **(V)** in inert solvents such as halocarbons to yield the desired ureas of general formula **(I)** wherein $R^1 = R^2 = H$:

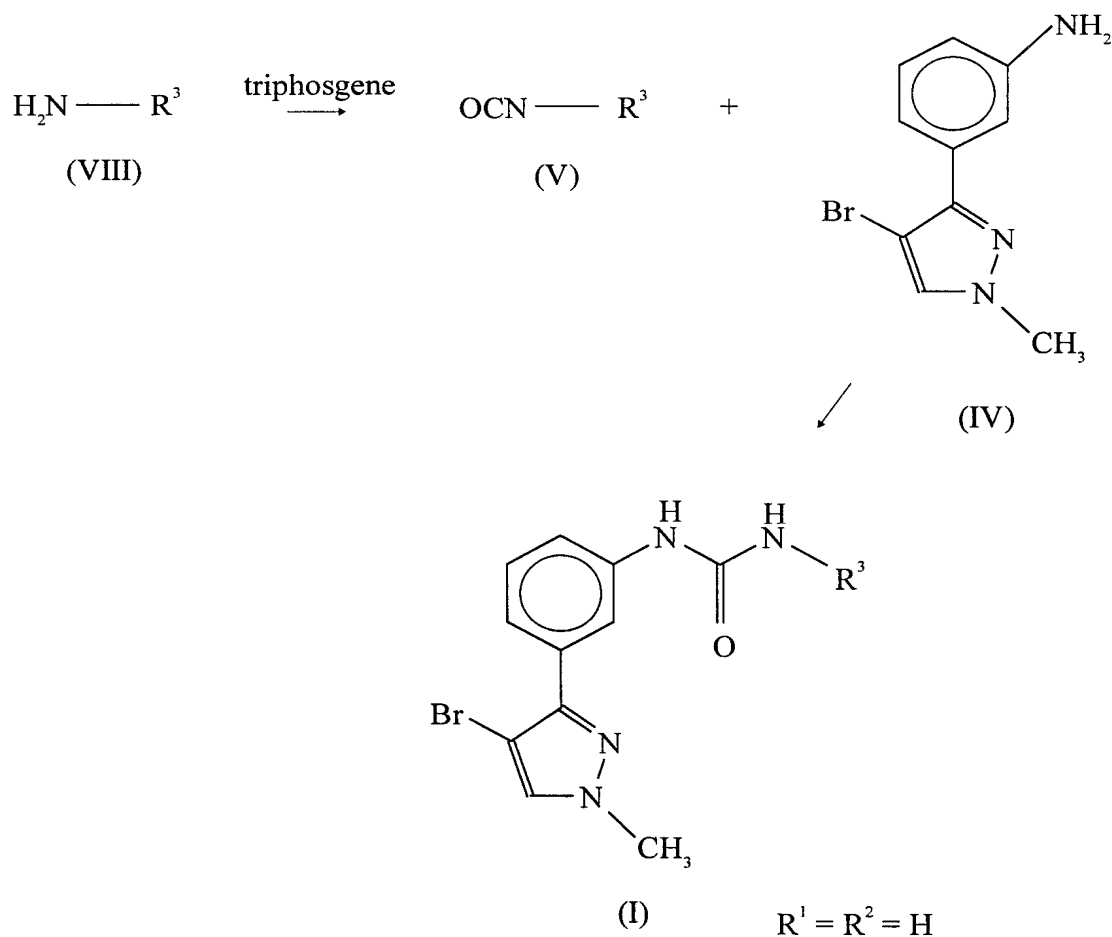


Alternatively the amine **(IV)** can be converted to the corresponding isocyanate **(VI)** by the action of phosgene or a suitable phosgene equivalent, e.g. triphosgene, in an inert solvent such as a halocarbon in the presence of an organic base such as triethylamine or ethyldiisopropylamine. Isocyanate **(VI)** reacts with amines of general formula **(VII)**, in an analogous fashion to that described above for the reaction of **(IV)** with **(V)**, yielding the desired ureas of general formula **(I)** wherein $R^1 = H$:

56

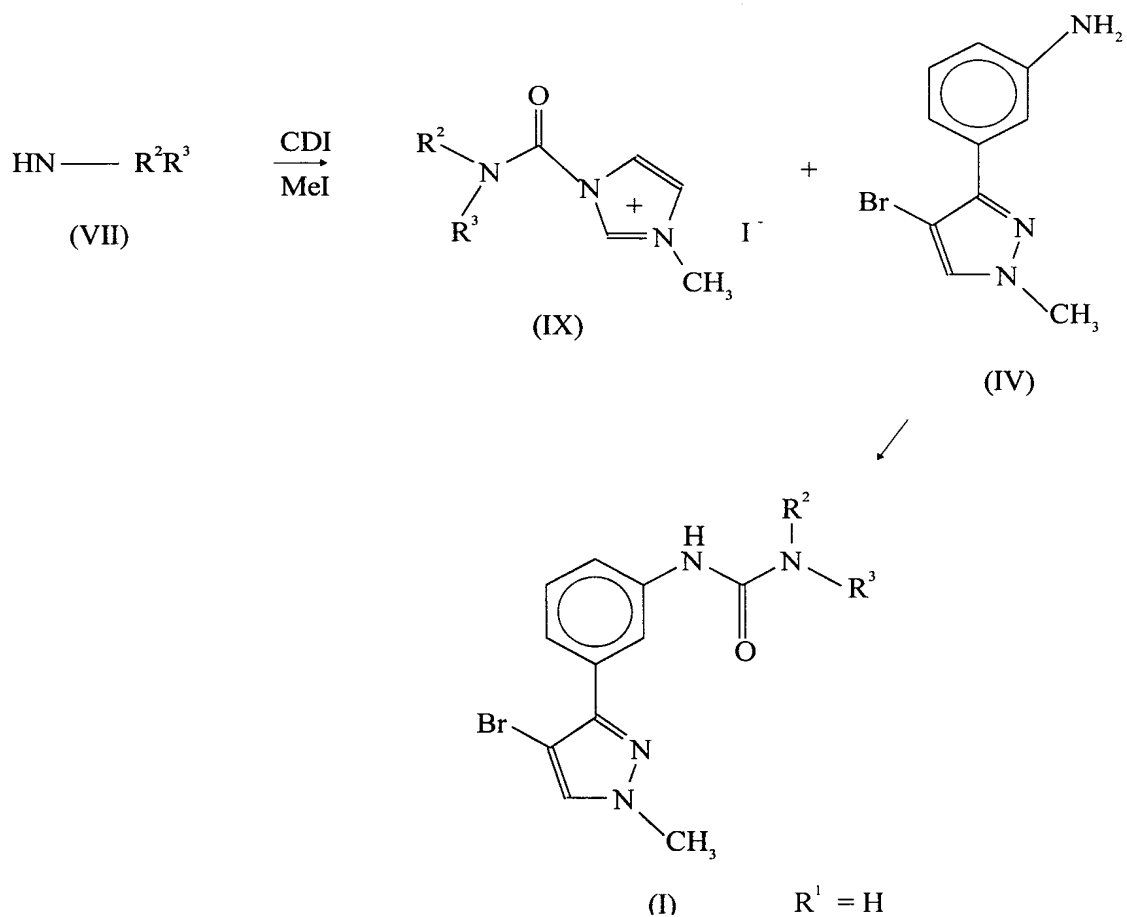


Alternatively wherein the isocyanate of general formula (V) is not commercially available it can be prepared from the corresponding amine of general formula (VIII) in an analogous procedure to that described above for the preparation of (VI). Reaction of these isocyanates with (IV) would again yield the requisite ureas of general formula (I) wherein $\text{R}^1 = \text{R}^2 = \text{H}$:

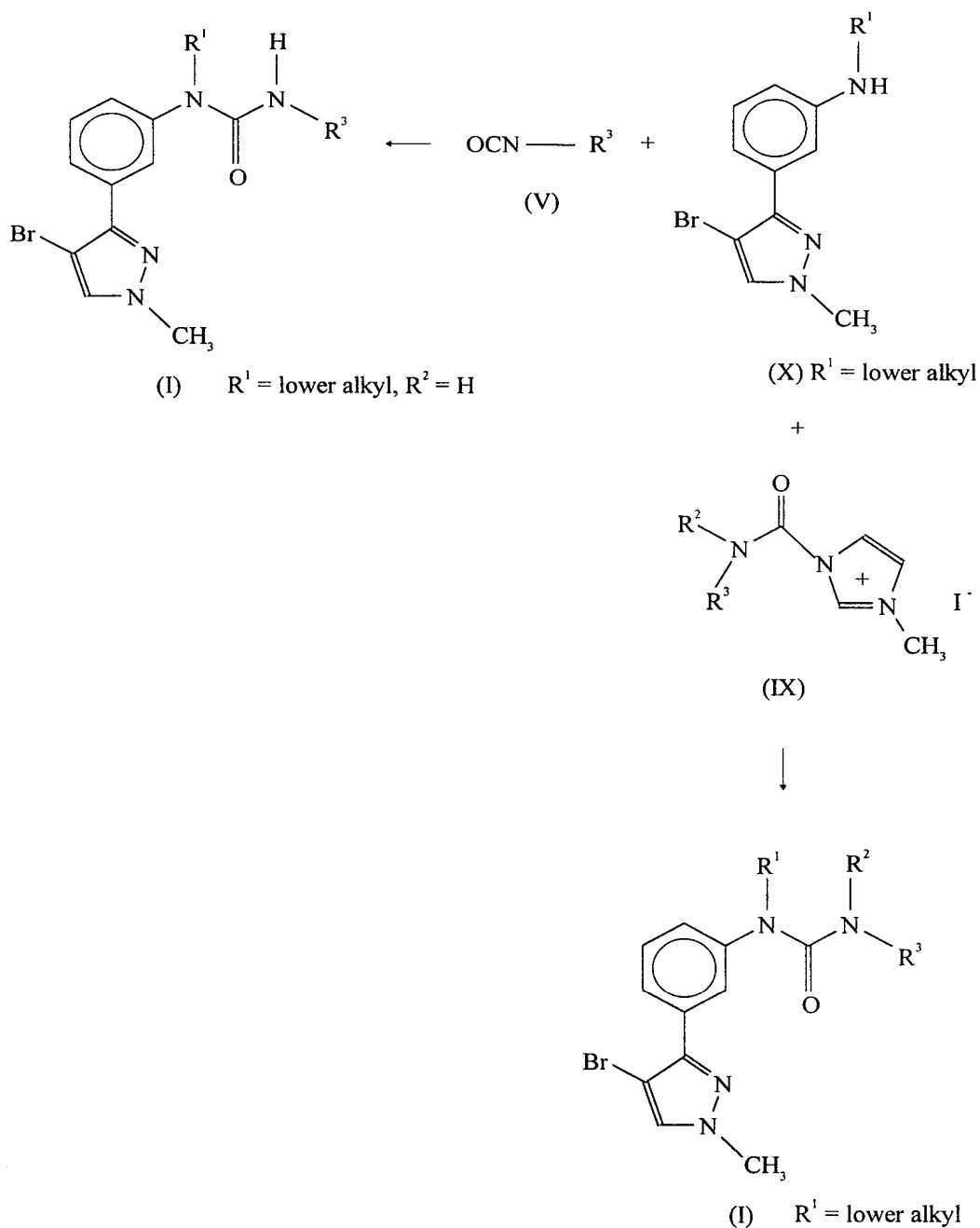


Amines of general formula (VII) are also readily converted to activated isocyanate equivalents of general formula (IX) by the sequential action of carbonyldiimidazole and methyl iodide in tetrahydrofuran and acetonitrile respectively (R.A. Batey *et al*, *Tetrahedron Lett.*, (1998), 39, 6267-6270.) Reaction of (IX) with (IV) in an inert solvent such as a halocarbon would yield the requisite ureas of general formula (I) wherein $\text{R}^1 = \text{H}$:

58

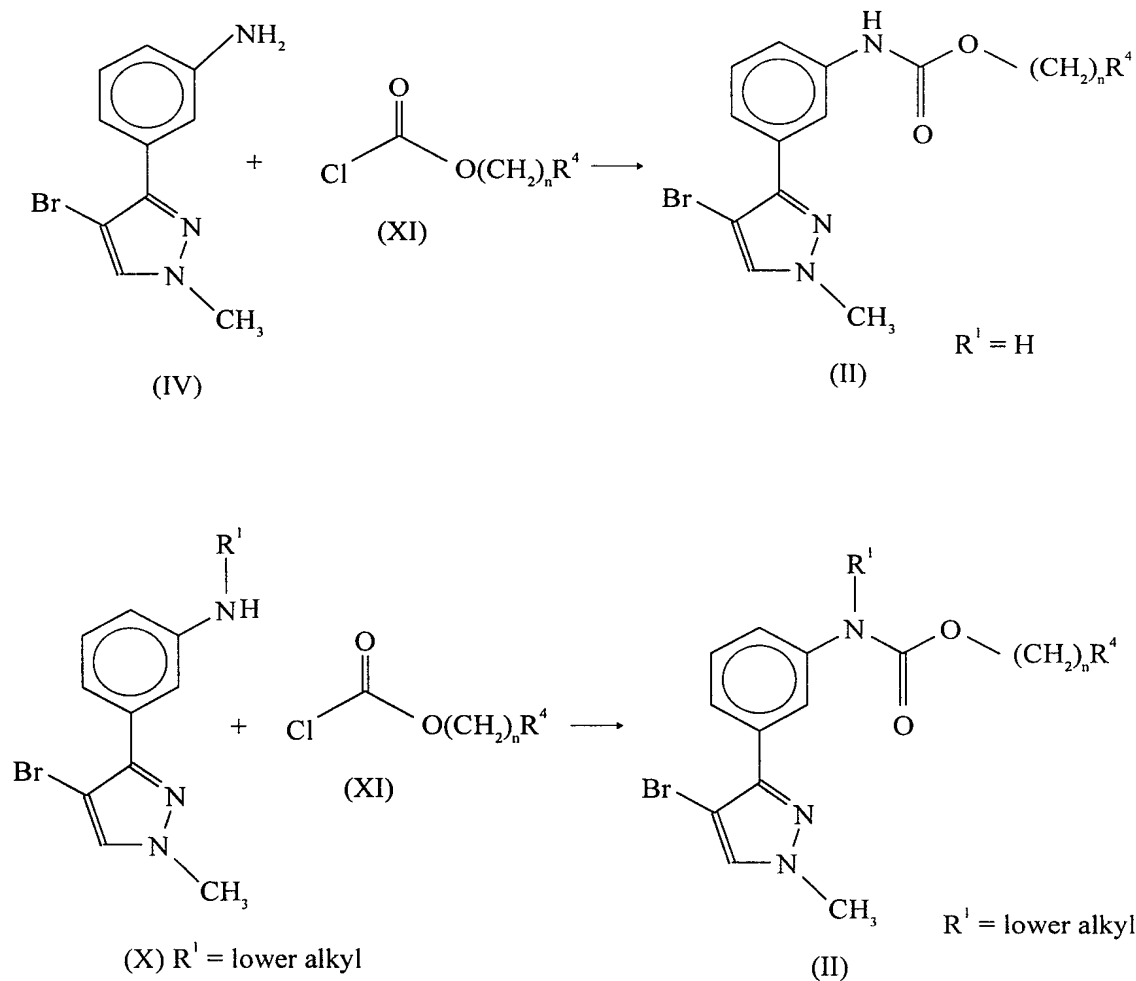


Amine (IV) may be monomethylated according to the procedure of J. Barluenga *et al*, *J. Chem. Soc., Chem. Commun.*, (1984), 20, 1334-1335, or alkylated according to the procedure of P. Marchini *et al*, *J. Org. Chem.*, (1975), 40(23), 3453-3456, to yield compounds of general formula (X) wherein R¹ = lower alkyl. These materials may be reacted as above with reagents of general formula (V) and (IX) as depicted below:



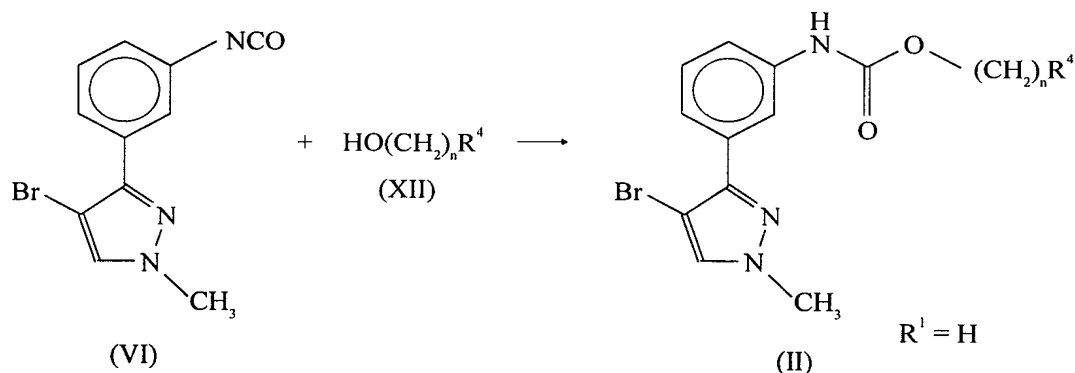
Compounds of general formula (II) can similarly be obtained *via* a variety of synthetic manipulations, all of which would be familiar to one skilled in the art. The reaction of amine (IV) with chloroformates (see Org. Syn. Coll. Vol. IV, (1963), 780) of general formula (XI) in an inert solvent such as ether or halocarbon in the presence of a tertiary base such as triethylamine or ethyldiisopropylamine readily yields the requisite carbamates of general formula (II) wherein $\text{R}^1 =$

H. Analogously amines of general formula (X) react similarly with chloroformates (XI) to yield the requisite carbamates of general formula (II) wherein R^1 = lower alkyl:

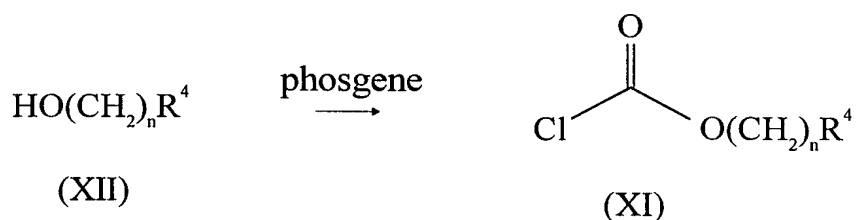


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An alternative route employs the ready reaction of an alcohol with an isocyanate. Thus isocyanate (VI) described previously reacts readily with alcohols (XII) in an aprotic solvent such as ether or chlorocarbon to yield the desired carbamates of general formula (II) wherein $R^1 = H$:



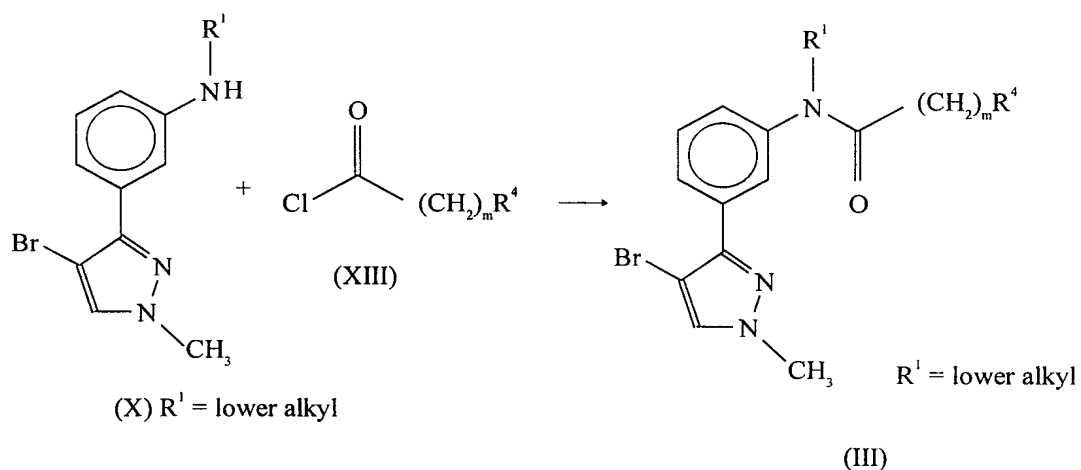
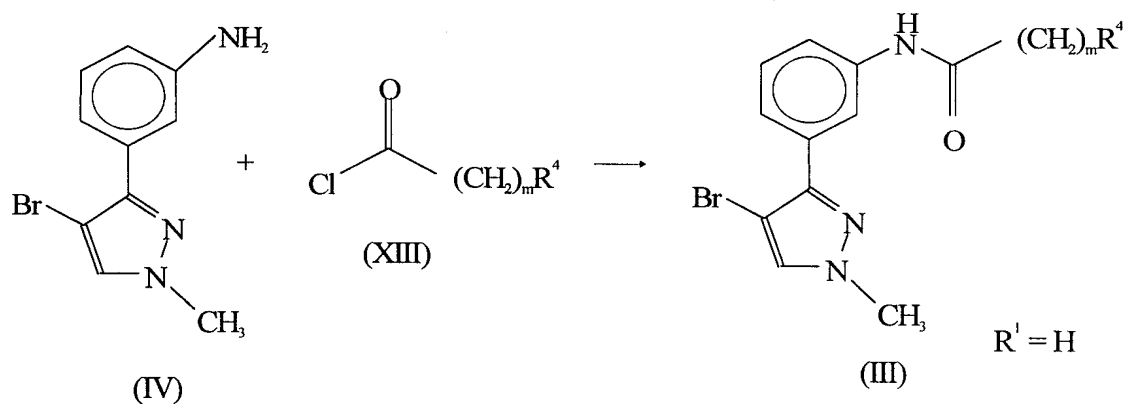
Chloroformates of general formula **(XI)** not commercially available may be readily prepared from the corresponding alcohol **(XII)** in an inert solvent such as toluene, chlorocarbon or ether by the action of excess phosgene (see Org. Syn. Coll. Vol. III, (1955), 167):



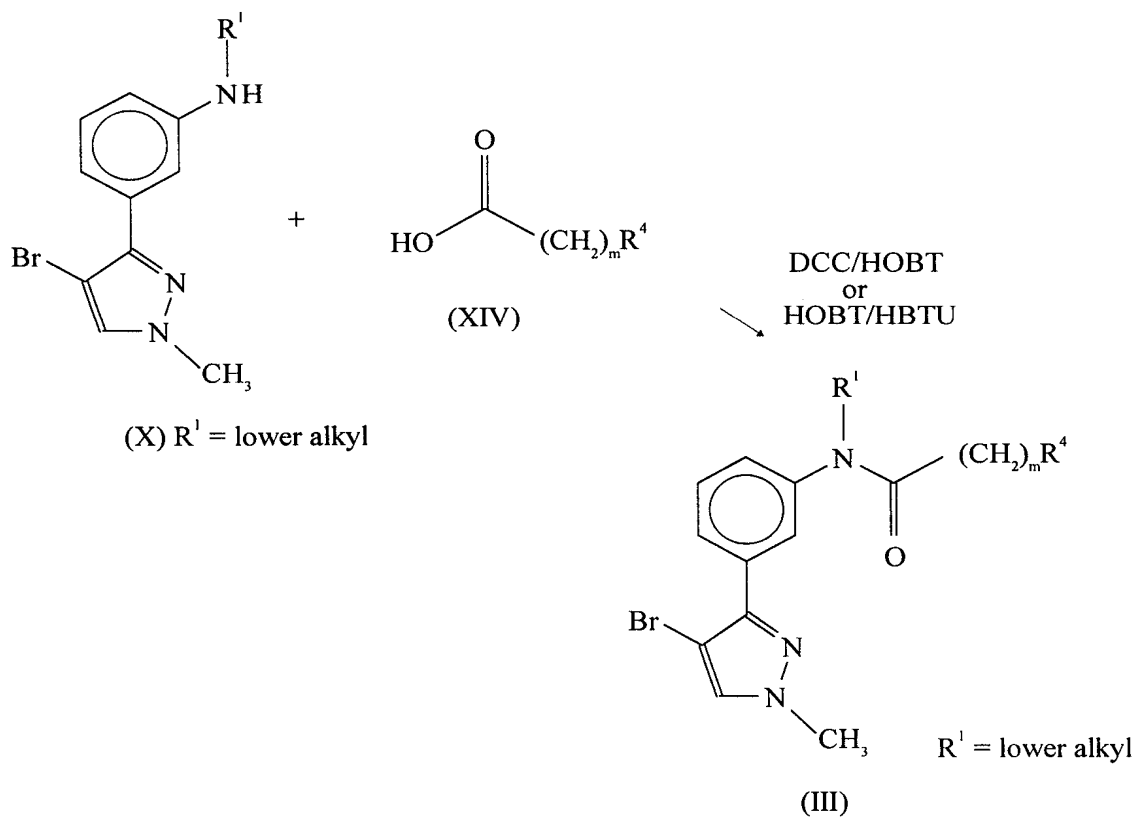
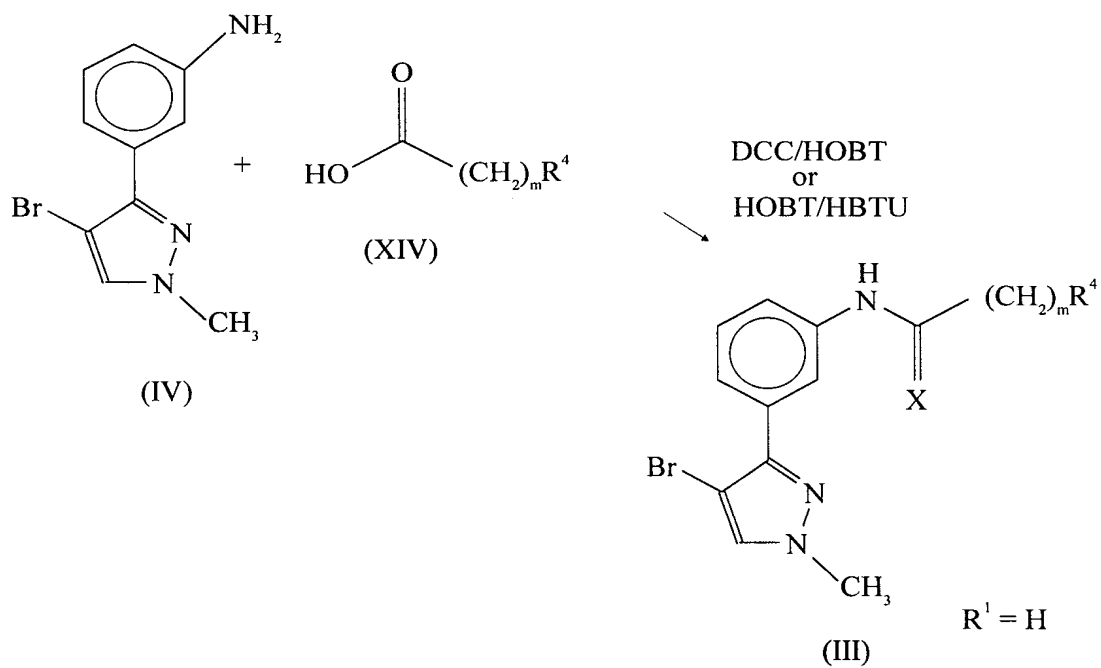
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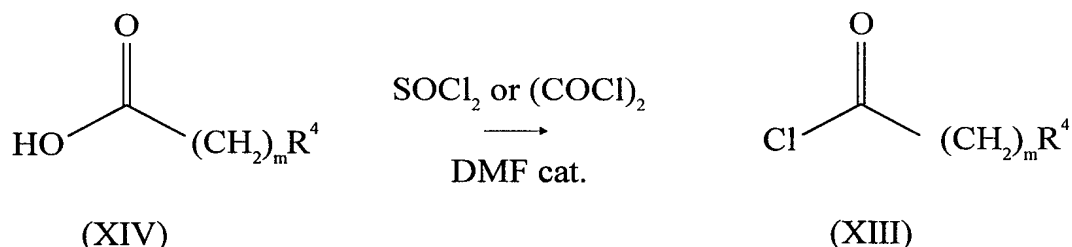
Compounds of general formula **(III)** can be obtained *via* a variety of synthetic manipulations, all of which would be familiar to one skilled in the art. The reaction of amine **(IV)** with acid chlorides (see Org. Syn. Coll. Vol. V, (1973), 336) of general formula **(XIII)** to yield the desired amides **(III)** wherein $\text{R}^1 = \text{H}$ is readily achieved in an inert solvent such as chloroform or dichloromethane in the presence of an organic base such as triethylamine or ethyldiisopropylamine. In an identical fashion amines of general formula **(X)** would react with acid chlorides **(XIII)** to yield the desired amides **(III)** wherein $\text{R}^1 = \text{lower alkyl}$:



Alternatively the corresponding acids of general formula (XIV) may be coupled with
 5 dicyclohexylcarbodiimide (DCC)/hydroxybenzotriazole (HOBt) (see W. König *et al*, *Chem. Ber.*,
 (1970), 103, 788) or hydroxybenzotriazole (HOBt)/2-(1H-benzotriazole-1-yl)-1,1,3,3-
 tetramethyluronium hexafluorophosphate (HBTU) (see M. Bernatowicz *et al.*, *Tetrahedron Lett.*,
 (1989), 30, 4645) as condensing agents in dimethylformamide or chloroform to amines (IV) and
 (X) respectively yielding products identical to those described in the previous scheme:



The acids of general formula (XIV) are readily converted to the corresponding acid chlorides (XIII) by the action of thionyl chloride or oxalyl chloride in the presence of catalytic dimethylformamide:



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A third aspect of the present invention provides a compound of formula (A) or a solvate or physiologically functional derivative thereof for use as a therapeutic agent, specifically as a modifier of the activity of the serotonin 5-HT_{2A} receptor. Modifiers of the activity of the serotonin 5-HT_{2A} receptor are believed to be of potential use for the treatment or prophylaxis of CNS, gastrointestinal, cardiovascular, and inflammatory disorders. Compounds of the formula (A) may be administered by oral, sublingual, parenteral, rectal, or topical administration. In addition to the neutral forms of compounds of formula (A) by appropriate addition of an ionizable substituent, which does not alter the receptor specificity of the compound, physiologically acceptable salts of the compounds may also be formed and used as therapeutic agents. Different amounts of the compounds of formula (A) will be required to achieve the desired biological effect. The amount will depend on factors such as the specific compound, the use for which it is intended, the means of administration, and the condition of the treated individual. A typical dose may be expected to fall in the range of 0.001 to 200 mg per kilogram of body weight of the treated individual. Unit does may contain from 1 to 200 mg of the compounds of formula (A) and may be administered one or more times a day, individually or in multiples. In the case of the salt or solvate of a compound of formulas (A), the dose is based on the cation (for salts) or the unsolvated compound.

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A fourth aspect of the present invention provides pharmaceutical compositions comprising at least one compound of formula (A) and/or a pharmacologically acceptable salt or solvate thereof as an active ingredient combined with at least one pharmaceutical carrier or excipient. Such pharmaceutical compositions may be used in the treatment of clinical conditions for which a modifier of the activity of the serotonin 5-HT_{2A} receptor is indicated. At least one compound of formula (A) may be combined with the carrier in either solid or liquid form in a unit dose formulation. The pharmaceutical carrier must be compatible with the other ingredients in the composition and must be tolerated by the individual recipient. Other physiologically active ingredients may be incorporated into the pharmaceutical composition of the invention if desired, and if such ingredients are compatible with the other ingredients in the composition. Formulations may be prepared by any suitable method, typically by uniformly mixing the active compound(s) with liquids or finely divided solid carriers, or both, in the required proportions, and then, if necessary, forming the resulting mixture into a desired shape.

Conventional excipients, such as binding agents, fillers, acceptable wetting agents, tableting lubricants, and disintegrants may be used in tablets and capsules for oral administration. Liquid preparations for oral administration may be in the form of solutions, emulsions, aqueous or oily suspensions, and syrups. Alternatively, the oral preparations may be in the form of dry powder which can be reconstituted with water or another suitable liquid vehicle before use. Additional additives such as suspending or emulsifying agents, non-aqueous vehicles (including edible oils), preservatives, and flavorings and colorants may be added to the liquid preparations. Parenteral dosage forms may be prepared by dissolving the compound of the invention in a suitable liquid vehicle and filter sterilizing the solution before filling and sealing an appropriate vial or ampoule. These are just a few examples of the many appropriate methods well known in the art for preparing dosage forms.

The fifth aspect of the present invention provides for the use of a compound of formula (A) in the preparation of a medicament for the treatment of a medical condition for which a modifier of the activity of the serotonin 5-HT_{2A} receptor is indicated.

A sixth aspect of the present invention provides for a method of treatment of a clinical condition of a mammal, such as a human, for which a modifier of the activity of the serotonin 5-HT_{2A} receptor is indicated, which comprises the administration to the mammal

of a therapeutically effective amount of a compound of formula (A) or a physiologically acceptable salt, solvate, or physiologically functional derivative thereof.

Experimental Data

5 Mass spectra were recorded on a Micromass Platform LC with Gilson HPLC. Infra-red spectra were recorded on a Nicolet Avatar 360 FT-IR. Melting points were recorded on a Electrothermal IA9200 apparatus and are uncorrected. Proton nuclear magnetic resonance spectra were recorded on a Bruker 300MHz machine. Chemical shifts are given with respect to tetramethylsilane. In the text the following abbreviations are used; s (singlet), d (doublet),
10 t (triplet), m (multiplet) or combinations thereof. Chemical shifts are quoted in parts per million (ppm) and with coupling constants in Hertz.

Thin layer chromatography was carried out using aluminium backed silica plates (250 μ L; GF₂₅₄). HPLC was recorded either on a HP Chemstation 1100 HPLC using a Hichrom 3.5 C18 reverse phase column (50mm x 2.1mm i.d.). Linear gradient elution over
15 5 minutes – 95% water (+0.1% TFA) / 5% acetonitrile (+0.05% TFA) down to 5% water / 95% acetonitrile. Flow rate 0.8mL/min [Method A]; or on a Hichrom 3.5 C18 reverse phase column (100mm x 3.2mm i.d.). Linear gradient elution over 11 minutes – 95% water (+0.1% TFA) / 5% acetonitrile (+0.05% TFA) down to 5% water / 95% acetonitrile. Flow rate 1mL/min [Method B]. Samples were routinely monitored at 254nm unless otherwise
20 stated.

All reagents were purchased from commercial sources.

Experiment 1

Preparation and Analysis of 103487

25 N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][(4-trifluoromethoxy)phenyl]amino] carboxamide

This compound is commercially available from Maybridge Chemical Company, Catalog No. KM04515.

Experiment 2

Preparation and Analysis of 116100

30 N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][4-methoxyphenoxy]carboxamide

To 4-methoxyphenylchloroformate (19mg, 0.10mmol) in CH₂Cl₂ (0.5mL) was added dropwise a solution of 3-(3-aminophenyl)-4-bromo-1-methylpyrazole (25mg, 0.10mmol) and triethylamine (14 μ L, 0.10mmol) in CH₂Cl₂ (0.5mL). The mixture was stirred for 16 h and

concentrated. Chromatography on flash silica (40% EtOAc/hexane) gave the title compound as a colourless solid (21mg, 52%), m.p. 140.3-141.8°C (EtOAc/hexane).

IR: ν_{\max} = 1748, 1592, 1504, 1412, 1190, 835, 764, 676 cm^{-1} . MS (ES+): m/z (%) = 404 (M+H ^{81}Br , 100), 402 (M+H ^{79}Br , 90).

$^1\text{H-NMR}$ (CD_3OD): δ = 3.80 (3H, s, CH_3), 3.81 (3H, s, CH_3), 6.91-6.98 (2H, m, ArH), 7.07-7.18 (3H, m, ArH), 7.42-7.53 (4H, m, ArH). HPLC: retention time 3.28 mins [Method A]. Tlc : Rf 0.4 (EtOAc/hexane).

Experiment 3

Preparation and Analysis of 116101

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][4-trifluoromethoxyphenyl]carboxamide

To 4-(trifluoromethoxy)benzoyl chloride (19 μL , 0.12mmol) in CH_2Cl_2 (1mL) was added dropwise a solution of 3-(3-aminophenyl)-4-bromo-1-methylpyrazole (30mg, 0.12mmol) and triethylamine (17 μL , 0.12mmol) in CH_2Cl_2 (0.5mL). The reaction mixture was stirred for 16 h and concentrated. Chromatography on flash silica (50% EtOAc/hexane) gave the title compound as a colourless solid (40mg, 76%), m.p. 138.6-139.6°C (EtOAc/hexane).

MS (ES+): m/z (%) = 442 (M+H ^{81}Br , 93), 440 (M+H ^{79}Br , 100).

$^1\text{H-NMR}$ ($\text{DMSO } d_6$): δ = 3.79 (3H, s, CH_3), 7.27 (1H, m, ArH), 7.45-7.60 (3H, m, ArH), 7.65 (1H, s, ArH), 7.87 (2H, m, ArH), 8.09 (2H, m, ArH), 10.51 (1H, s, NH).

HPLC: retention time 3.60 min [Method A]. TLC: Rf 0.40 (50% EtOAc/hexane).

Experiment 4

Preparation and Analysis of 116102

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][2-thienyl]carboxamide

To thiophene-2-carbonyl chloride (11 μL , 0.09mmol) in CH_2Cl_2 (1mL) was added dropwise a solution of 3-(3-aminophenyl)-4-bromo-1-methylpyrazole (25mg, 0.09mmol) and triethylamine (14 μL , 0.09mmol) in CH_2Cl_2 (0.5mL). The reaction mixture was stirred for 16 h and concentrated. Chromatography on flash silica (50% EtOAc/hexane) gave the title compound as a colourless solid (24mg, 68%), m.p. 127.8-128.6°C (EtOAc/hexane).

MS (ES+): m/z (%) = 364 (M+H ^{81}Br , 96), 362 (M+H ^{79}Br , 100).

¹H-NMR (CD₃OD): δ = 3.81 (3H, s, CH₃), 7.19 (2H, m, ArH), 7.48-7.58 (2H, m, ArH), 7.68-7.83 (3H, m, ArH), 7.93 (1H, dd, J=1.0, 3.8, ArH).

HPLC: retention time 3.12 min [Method A]. TLC: R_f 0.30 (30% EtOAc/hexane).

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Experiment 5

Preparation and Analysis of 116115

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][(4-trifluoromethoxy)phenyl)methyl]amino]carboxamide

To a stirred solution of triphosgene (12mg, 0.04mmol) in CH₂Cl₂ (0.5mL) was added dropwise a solution of 3-(3-aminophenyl)-4-bromo-1-methylpyrazole (30mg, 0.12mmol) and triethylamine (33μL, 0.24mmol) in CH₂Cl₂ (0.5mL). After 1 h, 4-(trifluoromethoxy)benzylamine (23mg, 0.12mmol) was added. The reaction mixture was stirred for 16 h and concentrated. Chromatography on flash silica (75%EtOAc/hexane) gave the title compound as a colourless solid (38mg, 68%), m.p. 144.6-145.8°C (EtOAc/hexane).

15 IR: ν_{max} = 1626, 1558, 1278, 1160, 969, 871, 789, 703 cm⁻¹. MS (ES⁺): m/z (%) = 471 (M+H ⁸¹Br, 91), 469 (M+H ⁷⁹Br, 100).

¹H-NMR (CD₃OD): δ = 3.81 (3H, s, CH₃), 4.42 (2H, s, CH₂), 7.06 (1H, d, J=7.1, ArH), 7.24 (2H, d, J=8.4, ArH), 7.37-7.52 (6H, m, ArH). HPLC: retention time 3.06 mins [Method A]. Tlc: R_f 0.5 (EtOAc).

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Experiment 6

Preparation and Analysis of 116120

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][4-chlorophenyl]carboxamide

To 4-chlorobenzoyl chloride (15mg, 0.08mmol) in CH₂Cl₂ (1mL) was added dropwise a solution of 3-(3-aminophenyl)-4-bromo-1-methylpyrazole (21mg, 0.08mmol) and triethylamine (12μL, 0.08mmol) in CH₂Cl₂ (0.5mL). The mixture was stirred for 16 h and concentrated. Chromatography on flash silica (50% EtOAc/hexane) gave the title compound as a colourless solid (23mg, 72%), m.p. 184.4-184.8°C (EtOAc/hexane).

30 MS (ES⁺): m/z (%) = 394 (M+H ⁸¹Br ³⁷Cl, 34), 392 (M+H ⁷⁹Br ³⁷Cl (⁸¹Br ³⁵Cl), 100), 390 (M+H ⁷⁹Br ³⁵Cl, 67).

¹H-NMR (DMSO d₆): δ = 3.79 (3H, s, CH₃), 7.25 (1H, d, J=7.9, ArH), 7.51-7.65 (3H, m, ArH), 7.69 (1H, s, ArH), 7.90 (2H, m, ArH), 8.00 (2H, m, ArH), 10.51 (1H, s, NH).

HPLC: retention time 3.40 min [Method A]. TLC: R_f 0.35 (50% EtOAc/hexane).

Experiment 7

Preparation and Analysis of 116137

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]-2-[4-(trifluoromethoxy)phenyl]acetamide

5 A solution of 3-(3-aminophenyl)-4-bromo-1-methylpyrazole (35mg, 0.14mmol) and triethylamine (23 μ L, 0.17mmol) in DMF (0.5mL) was added in one portion to a stirred solution of 4-trifluoromethoxyphenylacetic acid (31mg, 0.14mmol), HBTU (53mg, 0.14mmol) and HOBT (19mg, 0.14mmol) in DMF (1mL). The mixture was heated at 70°C
10 for 24 h and then quenched with aqueous sodium bicarbonate solution. Ethyl acetate was added and the organic phase separated, washed with water (x3), brine, dried (MgSO₄) and evaporated. Chromatography on flash silica (50%EtOAc/hexane) gave the title compound as a colourless solid (43mg, 68%), m.p. 141.2-142.5°C (EtOAc/hexane).

IR: ν_{\max} = 1684, 1592, 1510, 1253, 1217, 1157, 987, 798, 700 cm⁻¹.

15 MS (ES⁺): m/z (%) = 456 (M+H ⁸¹Br, 100), 454 (M+H ⁷⁹Br, 94).

¹H-NMR (DMSO d₆): δ = 3.72 (2H, s, CH₂), 3.75 (3H, s, CH₃), 7.17 (1H, d, J=7.7, ArH), 7.33 (2H, d, J=8.7, ArH), 7.38-7.51 (3H, m, ArH), 7.62-7.73 (3H, m, ArH), 10.44 (1H, s, NH).

HPLC: retention time 3.52 min [Method A].

Experiment 8

Preparation and Analysis of 116174

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]-2-(3-fluorophenyl)acetamide

25 A mixture of 3-(3-aminophenyl)-4-bromo-1-methylpyrazole (30 mg, 0.12 mmol), 3-fluorophenylacetic acid (18 mg, 0.12 mmol), 1-hydroxybenzotriazole hydrate (16 mg, 0.12 mmol) and 2-(1H-benzotriazole-1-yl)-1,1,3,3-tetramethyluronium hexafluoro-phosphate (46 mg, 0.12 mmol) were dissolved in chloroform (1.5 ml). N, N-Diisopropylethylamine (0.02 ml, 0.13 mmol) was added and the mixture stirred at room temperature for 16h. The
30 reaction mixture was then poured into brine and the organic layer washed with further brine, dried over magnesium sulphate and then concentrated in vacuo. The crude product was purified by column chromatography (ethyl acetate-toluene, 1:1), giving the title compound (12 mg, 26 %). R_f 0.41 (ethyl acetate-toluene, 1:1).

HPLC (Method B): retention time 7.07 min (100 %). δ_H ($CDCl_3$) 3.77 (2H, s), 3.83 (3H, s), 7.02 – 7.20 (4H, m), 7.54 (1H, s), 7.60 – 7.63 (1H, m). MS (AP+): m/z (%) = 390 (M + H ^{81}Br , 100), 388 (M + H ^{79}Br , 100).

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Experiment 9

Preparation and Analysis of 116175

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]-2-(3-methoxyphenyl)acetamide

A solution of 3-methoxyphenylacetyl chloride (0.02 ml, 0.12 mmol) in
10 dichloromethane (0.75 ml) was added dropwise at 0 °C to a solution of 3-(3-aminophenyl)-
4-bromo-1-methylpyrazole (30 mg, 0.12 mmol) and triethylamine (0.02 ml, 0.13 mmol) in
dichloromethane (0.75 ml). The resulting mixture was stirred at room temperature for 16h
and then poured into brine. The organic layer was washed with more brine then dried over
magnesium sulphate and concentrated *in vacuo*. The crude product was purified by column
15 chromatography (ethyl acetate-toluene, 1:1), giving the title compound (9 mg, 19 %). Rf
0.30 (ethyl acetate-toluene, 1:1).

HPLC (Method B): retention time 8.62 min (97.09 %). δ_H ($CDCl_3$) 3.76 (2H, s),
3.82 (3H, s), 3.85 (3H, s), 6.84 – 6.90 (3H, m), 7.07 – 7.44 (5H, m), 7.53 (1H, s), 7.60 (1H,
br s). MS (AP+): m/z (%) = 402 (M + H ^{81}Br , 100), 400 (M + H ^{79}Br , 95).

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Experiment 10

Preparation and Analysis of 116176

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]-2-(2-fluorophenyl)acetamide

25 A mixture of 3-(3-aminophenyl)-4-bromo-1-methylpyrazole (30 mg, 0.12 mmol), 2-
fluorophenylacetic acid (18 mg, 0.12 mmol), 1-hydroxybenzotriazole hydrate (16 mg, 0.12
mmol) and 2-(1H-benzotriazole-1-yl)-1,1,3,3-tetramethyluronium hexafluoro-phosphate (46
mg, 0.12 mmol) were dissolved in chloroform (1.5 ml). N, N-Diisopropylethylamine (0.02
ml, 0.13 mmol) was added and the mixture stirred at room temperature for 16h. The
30 reaction mixture was then poured into brine and the organic layer washed with further brine,
dried over magnesium sulphate and then concentrated *in vacuo*. The crude product was
purified by column chromatography (ethyl acetate-toluene, 1:1), giving the title compound
(15 mg, 32 %). Rf 0.52 (ethyl acetate-toluene, 1:1).

HPLC (Method B): retention time 7.28 min (100 %). δ_H ($CDCl_3$) 3.79 (2H, s), 3.83 (3H, s), 7.11 – 7.23 (3H, m), 7.30 – 7.55 (6H, m), 7.61 – 7.64 (1H, m). MS (AP+): m/z (%) = 390 (M + H ^{81}Br , 100), 388 (M + H ^{79}Br , 100).

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Experiment 11

Preparation and Analysis of 116177

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]-2-(4-nitrophenyl)acetamide

A mixture of 3-(3-aminophenyl)-4-bromo-1-methylpyrazole (30 mg, 0.12 mmol), 4-nitrophenylacetic acid (22 mg, 0.12 mmol), 1-hydroxybenzotriazole hydrate (16 mg, 0.12 mmol) and 2-(1H-benzotriazole-1-yl)-1,1,3,3-tetramethyluronium hexafluorophosphate (46 mg, 0.12 mmol) were dissolved in chloroform (1.5 ml). N, N-Diisopropylethylamine (0.02 ml, 0.13 mmol) was added and the mixture stirred at room temperature for 16h. The reaction mixture was then poured into brine and the organic layer washed with further brine, dried over magnesium sulphate and then concentrated in vacuo. The crude product was purified by column chromatography (ethyl acetate-toluene, 1:1), giving the title compound (9 mg, 18 %). Rf 0.19 (ethyl acetate-toluene, 1:1).

HPLC (Method B): retention time 7.22 min (94.30 %). δ_H ($CDCl_3$) 3.83 (3H, s), 3.87 (2H, s), 7.18 – 7.23 (1H, m), 7.42 – 7.65 (7H, m), 8.22 – 8.30 (2H, m). MS (AP+): m/z (%) = 417 (M + H ^{81}Br , 100), 415 (M + H ^{79}Br , 100).

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Experiment 12

Preparation and Analysis of 116178

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]-2-(2-methoxyphenyl)acetamide

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A mixture of 3-(3-aminophenyl)-4-bromo-1-methylpyrazole (30 mg, 0.12 mmol), 2-methoxyphenylacetic acid (20 mg, 0.12 mmol), 1-hydroxybenzotriazole hydrate (16 mg, 0.12 mmol) and 2-(1H-benzotriazole-1-yl)-1,1,3,3-tetramethyluronium hexafluorophosphate (46 mg, 0.12 mmol) were dissolved in chloroform (1.5 ml). N, N-Diisopropylethylamine (0.02 ml, 0.13 mmol) was added and the mixture stirred at room temperature for 16h. The reaction mixture was then poured into brine and the organic layer washed with further brine, dried over magnesium sulphate and then concentrated in vacuo. The crude

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product was purified by column chromatography (chloroform-methanol, 99:1), giving the title compound (18 mg, 38 %) as a colourless solid. R_f 0.65 (chloroform-methanol, 98:2).

HPLC (Method B): retention time 7.16 min (100 %). δ_{H} (CDCl₃) 3.76 (2H, s), 3.83 (3H, s), 3.98 (3H, s), 6.97 – 7.06 (2H, m), 7.11 – 7.16 (1H, m), 7.31 – 7.50 (4H, m), 7.53 (1H, s), 7.57 – 7.60 (1H, m), 7.91 (1H, br s). MS (AP-): m/z (%) = 400 (M – H ⁸¹Br, 90), 398 (M – H ⁷⁹Br, 100).

Experiment 13

Preparation and Analysis of 116192

10 {[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(1,1-dimethylethoxy)carboxamide

To di-*tert*-butyl dicarbonate (36mg, 0.17mmol) in methanol (1mL) was added dropwise a solution of 3-(3-aminophenyl)-4-bromo-1-methylpyrazole (42mg, 0.17mmol) in methanol (1mL). The mixture was stirred for 16 h and concentrated. Chromatography on flash silica (40%EtOAc/heaxne) gave the title compound as a colourless solid (29mg, 49%)
15 (EtOAc/hexane).

MS (CI-): m/z (%) = 352 (M-H ⁸¹Br, 100), 350 (M-H ⁷⁹Br, 96).

¹H-NMR (DMSO d₆): δ = 1.46 (9H, s, 3xCH₃), 3.73 (3H, s, CH₃), 7.07 (1H, m, ArH), 7.42 (1H, t, J=7.7, ArH), 7.53-7.60 (2H, m, ArH), 7.64 (1H, s, ArH), 9.57 (1H, s, NH).

20 HPLC: retention time 7.15 min [Method B].

One or the other (as indicated) of the two following synthetic protocols was used to generate each of the compounds below:

Protocol A:

25 To an isocyanate (1mmol) in CH₂Cl₂ (4mL) was added dropwise a solution of 3-(3-aminophenyl)-4-bromo-1-methylpyrazole (1mmol) in CH₂Cl₂ (4mL). The mixture was stirred for 16 hours and concentrated. Chromatography on flash silica (20%-80% EtOAc/hexane) followed by recrystallisation gave the pure urea.

Protocol B:

30 To a stirred solution of triphosgene (0.33mmol) in CH₂Cl₂ (4mL) was added dropwise a solution of 3-(3-aminophenyl)-4-bromo-1-methylpyrazole (1mmol) and triethylamine (2mmol) in CH₂Cl₂ (4mL). After 1 hour, an aniline was added (1mmol). The

reaction mixture was stirred for 16 hours and concentrated. Chromatography on flash silica (20%-80%EtOAc/hexane) followed by recrystallisation gave the pure urea.

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Experiment 14

Preparation and Analysis of 116079

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][(4-methylthiophenyl)amino]carboxamide

[Protocol A] – 4-(methylthio)phenyl isocyanate

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colourless solid (EtOAc/hexane)

MS (ES⁺): m/z (%) = 419 (M+H ⁸¹Br, 100), 417 (M+H ⁷⁹Br, 94).

¹H-NMR (MeOH d₄): δ = 2.42 (3H, s, SCH₃), 3.81 (3H, s, NCH₃), 7.06 (1H, m, ArH), 7.22 (2H, m, ArH), 7.37 (2H, m, ArH), 7.42-7.61 (4H, m, ArH).

HPLC: retention time 3.35 min [Method A].

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Experiment 15

Preparation and Analysis of 116081

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][(4-chlorophenyl)amino]carboxamide

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[Protocol A] – 4-chlorophenyl isocyanate

colourless solid (EtOAc/hexane)

MS (ES⁺): m/z (%) = 409 (M+H ⁸¹Br ³⁷Cl, 19), 407 (M+H ⁷⁹Br ³⁷Cl (⁸¹Br ³⁵Cl), 100), 405 (M+H ⁷⁹Br ³⁵Cl, 81).

¹H-NMR (MeOH d₄): δ = 3.81 (3H, s, CH₃), 7.07 (1H, m, ArH), 7.23 (2H, m, ArH), 7.36-7.60 (6H, m, ArH).

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HPLC: retention time 3.42 min [Method A].

Experiment 16

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Preparation and Analysis of 116082

{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(4-fluorophenyl)carboxamide

[Protocol A] – 4-fluorophenyl isocyanate

colourless solid (EtOAc/hexane)

MS (ES⁺): m/z (%) = 391 (M+H ⁸¹Br, 96), 389 (M+H ⁷⁹Br, 100).

¹H-NMR (MeOH d₄): δ = 3.81 (3H, s, CH₃), 6.93-7.11 (3H, m, ArH), 7.37-7.61 (6H, m, ArH).

HPLC: retention time 3.11 min.

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Experiment 17

Preparation and Analysis of 116087

{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-[2-(trifluoromethoxy)phenyl]carboxamide
[Protocol A] - 2-(trifluoromethoxy)phenyl isocyanate

10 colourless solid (EtOAc/hexane)

MS (ES⁺): m/z (%) = 457 (M+H ⁸¹Br, 100), 455 (M+H ⁷⁹Br, 95).

¹H-NMR (DMSO d₆): δ = 3.79 (3H, s, CH₃), 7.06-7.18 (2H, m, ArH), 7.38-7.49 (2H, m, ArH), 7.51-7.62 (2H, m, ArH), 7.65 (1H, m, ArH), 7.71 (1H, s, ArH), 8.24 (1H, dd, J=1.1, 8.2, ArH), 8.56 (1H, s, NH), 9.49 (1H, s, NH).

15 HPLC: retention time 3.40 min.

Experiment 18

Preparation and Analysis of 116089

{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(2-nitrophenyl)carboxamide

20 [Protocol A] - 2-nitrophenyl isocyanate

yellow solid (EtOAc/hexane)

MS (ES⁺): m/z (%) = 418 (M+H ⁸¹Br, 98), 416 (M+H ⁷⁹Br, 100).

¹H-NMR (DMSO d₆): δ = ¹H-NMR (DMSO d₆): \square = 3.79 (3H, s, NCH₃), 7.14 (1H, m, ArH), 7.24 (1H, m, ArH), 7.50 (1H, t, J=7.7, ArH), 7.60 (2H, m, ArH), 7.67 (1H, s, ArH), 7.71 (1H, s, ArH), 8.10 (1H, m, ArH), 8.29 (1H, m, ArH), 9.65 (1H, s, NH), 10.09 (1H, s, NH).

HPLC: retention time 3.10 min [Method A].

Experiment 19

30

Preparation and Analysis of 116091

{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(4-methoxyphenyl)carboxamide

[Protocol A] - 4-methoxyphenyl isocyanate

colourless solid (EtOAc/hexane)

MS (ES+): m/z (%) = 403 (M+H ^{81}Br , 100), 401 (M+H ^{79}Br , 96).

^1H -NMR (DMSO d_6): δ = 3.71 (3H, s, OCH₃), 3.79 (3H, s, NCH₃), 6.87 (2H, d, J=8.9, ArH), 7.06 (1H, d, J=7.5, ArH), 7.39 (2H, d, J=8.9, ArH), 7.45-7.61 (3H, m, ArH), 7.65 (1H, s, ArH), 8.52 (1H, s, NH), 8.84 (1H, s, NH).

5 HPLC: retention time 3.08 min.

Experiment 20

Preparation and Analysis of 116092

{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(2-methylphenyl)carboxamide

10 [Protocol A] – *o*-tolyl isocyanate

colourless solid (EtOAc/hexane)

MS (ES+): m/z (%) = 387 (M+H ^{81}Br , 94), 385 (M+H ^{79}Br , 100).

^1H -NMR (MeOH d_4): δ = 2.29 (3H, s, CH₃), 3.81 (3H, s, NCH₃), 7.03 (1H, dt, J=1.1, 7.5, ArH), 7.09 (1H, dt, J=1.1, 7.5, ArH), 7.13-7.22 (2H, m, ArH), 7.45 (1H, t, J=7.9, ArH), 7.49-7.57 (2H, m, ArH), 7.60-7.68 (2H, m, ArH).

15

HPLC: retention time 2.96 min.

Experiment 21

Preparation and Analysis of 116097

20 {[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-[4-(trifluoromethyl)phenyl]carboxamide

[Protocol A] – 4-(trifluoromethyl)phenyl isocyanate

colourless solid (EtOAc/hexane)

MS (ES+): m/z (%) = 441 (M+H ^{81}Br , 94), 439 (M+H ^{79}Br , 100).

^1H -NMR (MeOH d_4): δ = 3.82 (3H, s, CH₃), 7.04-7.16 (3H, m, ArH), 7.20-7.47 (6H, m, ArH).

25

HPLC: retention time 3.56 min.

Experiment 22

Preparation and Analysis of 116105

30 {[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(3-chlorophenyl)carboxamide

[Protocol A] – 3-chlorophenyl isocyanate

colourless solid (EtOAc/hexane)

MS (ES⁺): m/z (%) = 409 (M+H ⁸¹Br ³⁷Cl, 26), 407 (M+H ⁷⁹Br ³⁷Cl (⁸¹Br ³⁵Cl), 100), 405 (M+H ⁷⁹Br ³⁵Cl, 70).

¹H-NMR (MeOH d₄): δ = 3.81 (3H, s, NCH₃), 7.04 (1H, m, ArH), 7.10 (1H, m, ArH), 7.28 (2H, m, ArH), 7.47 (1H, t, J=7.8, ArH), 7.55 (1H, m, ArH), 7.63 (1H, m, ArH),
5 7.68 (1H, s, ArH), 7.73 (1H, m, ArH), 9.04 (2H, s, NH).

HPLC: retention time 3.20 min [Method A].

Experiment 23

Preparation and Analysis of 116108

10 {[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(2-chlorophenyl)carboxamide
[Protocol A] – 2-chlorophenyl isocyanate
colourless solid (EtOAc/hexane)

MS (ES⁺): m/z (%) = 409 (M+H ⁸¹Br ³⁷Cl, 24), 407 (M+H ⁷⁹Br ³⁷Cl (⁸¹Br ³⁵Cl), 100), 405 (M+H ⁷⁹Br ³⁵Cl, 72).

15 ¹H-NMR (MeOH d₄): δ = 3.81 (3H, s, NCH₃), 7.03 (1H, m, ArH), 7.11 (1H, m, ArH), 7.28 (1H, m, ArH), 7.35-7.53 (3H, m, ArH), 7.55 (1H, s, ArH), 7.62 (1H, m, ArH), 8.11 (1H, m, ArH).

HPLC: retention time 3.13 min.

Experiment 24

Preparation and Analysis of 116110

20 {[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-[4-(methylethyl)phenyl]carboxamide
[Protocol A] – 4-isopropylphenyl isocyanate
colourless solid (THF/hexane)

25 MS (ES⁺): m/z (%) = 415 (M+H ⁸¹Br, 100), 413 (M+H ⁷⁹Br, 92).

¹H-NMR (MeOH d₄): δ = 1.23 (6H, d, J=6.8, 2xCH₃), 2.86 (1H, septet, J=6.8, CH), 3.82 (3H, s, NCH₃), 7.09 (1H, m, ArH), 7.16 (2H, d, J=7.6, ArH), 7.31 (2H, d, J=7.6, ArH), 7.42-7.51 (2H, m, ArH), 7.54 (1H, s, ArH), 7.59 (1H, m, ArH).

HPLC: retention time 3.66 min.

Experiment 25

Preparation and Analysis of 116111

30 {[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(3-methoxyphenyl)carboxamide

[Protocol A] – 3-methoxyphenyl isocyanate

colourless solid (EtOAc/hexane)

MS (ES⁺): m/z (%) = 403 (M+H ⁸¹Br, 100), 401 (M+H ⁷⁹Br, 96).

¹H-NMR (MeOH d₄): δ = 3.73 (3H, s, OCH₃), 3.81 (3H, s, NCH₃), 6.59 (1H, m, ArH), 6.91 (1H, m, ArH), 7.08 (1H, m, ArH), 7.14 (2H, m, ArH), 7.39-7.61 (4H, m, ArH).

HPLC: retention time 2.90 min.

Experiment 26

Preparation and Analysis of 116112

{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(3-methylphenyl)carboxamide

[Protocol A] – *m*-tolyl isocyanate

colourless solid (EtOAc/hexane)

MS (ES⁺): m/z (%) = 387 (M+H ⁸¹Br, 100), 385 (M+H ⁷⁹Br, 96).

¹H-NMR (DMSO d₆): δ = 2.26 (3H, s, CH₃), 3.76 (3H, s, NCH₃), 6.79 (1H, m, ArH), 7.06-7.22 (3H, m, ArH), 7.29 (1H, m, ArH), 7.43-7.62 (3H, m, ArH), 7.68 (1H, s, ArH), 8.65 (1H, s, NH), 8.89 (1H, s, NH).

HPLC: retention time 3.05 min [Method A].

Experiment 27

Preparation and Analysis of 116113

{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-methyl-N-[4-(trifluoromethoxy)phenyl]carboxamide

[Protocol B] – *N*-methyl-4-(trifluoromethoxy)aniline

pale yellow solid (EtOAc/hexane)

MS (ES⁺): m/z (%) = 471 (M+H ⁸¹Br, 88), 469 (M+H ⁷⁹Br, 100).

¹H-NMR (MeOH d₄): δ = 3.35 (3H, s, NCH₃), 3.81 (3H, s, NCH₃), 7.09 (1H, m, ArH), 7.25-7.51 (8H, m, ArH).

HPLC: retention time 3.56 min [Method A].

Experiment 28

Preparation and Analysis of 116119

N-[4-(*tert*-butyl)phenyl]{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}carboxamide

[Protocol B] – 4-*tert*-butylaniline

colourless solid (EtOAc/hexane)

MS (ES⁺): m/z (%) = 429 (M+H ⁸¹Br, 98), 427 (M+H ⁷⁹Br, 100).

¹H-NMR (DMSO d₆): δ = 1.27 (9H, s, 3xCH₃), 3.79 (3H, s, NCH₃), 7.07 (1H, d, J=7.5, ArH), 7.29 (2H, d, J=8.7, ArH), 7.37 (2H, d, J=8.7, ArH), 7.45 (1H, t, J=7.5, ArH),
5 7.51-7.60 (2H, m, ArH), 7.66 (1H, s, ArH), 8.65 (1H, s, NH), 8.83 (1H, s, NH).

HPLC: retention time 3.77 min.

Experiment 29

Preparation and Analysis of 116122

10 N-[4-(dimethylamino)phenyl]{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino} carboxamide
[Protocol B] – *N,N*-dimethyl-*p*-phenylenediamine

colourless solid (EtOAc/hexane)

MS (ES⁺): m/z (%) = 416 (M+H ⁸¹Br, 96), 414 (M+H ⁷⁹Br, 100).

¹H-NMR (DMSO d₆): δ = 2.86 (6H, s, NCH₃), 3.80 (3H, s, NCH₃), 6.80 (2H, m,
15 ArH), 7.09 (1H, d, J=7.7, ArH), 7.28 (2H, m, ArH), 7.42 (1H, t, J=7.8, ArH), 7.52 (1H, m,
ArH), 7.59 (1H, s, ArH), 7.67 (1H, s, ArH), 8.45 (1H, s, NH), 8.75 (1H, s, NH).

HPLC: retention time 2.07 min [Method A].

Experiment 30

20 Preparation and Analysis of 116138

N-(3,5-dichloro-4-methylphenyl){[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino} carboxamide
[Protocol B] – 3,5-dichloro-4-methylphenylamine

colourless solid (EtOAc/hexane)

MS (ES⁺): m/z (%) = 457 (M+H, 35), 455 (M+H, 100), 453 (M+H, 65).

¹H-NMR (DMSO d₆): δ = 2.32 (3H, s, CH₃), 3.79 (3H, s, NCH₃), 7.11 (1H, d, J=7.4,
25 ArH), 7.46 (1H, t, J=7.8, ArH), 7.50-7.64 (4H, m, ArH), 7.68 (1H, s, ArH), 9.02 (1H, s,
NH), 9.09 (1H, s, NH).

HPLC: retention time 3.66 min.

30

Experiment 31

Preparation and Analysis of 116139

{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-[4-(trifluoromethylthio)phenyl]carboxamide
[Protocol B] – 4-(trifluoromethylthio)aniline

colourless solid (EtOAc/hexane)

MS (ES+): m/z (%) = 473 (M+H ^{81}Br , 100), 471 (M+H ^{79}Br , 94).

$^1\text{H-NMR}$ (DMSO d_6): δ = 3.81 (3H, s, NCH₃), 7.11 (1H, d, J=7.5, ArH), 7.47 (1H, t, J=7.9, ArH), 7.51-7.63 (6H, m, ArH), 7.66 (1H, s, ArH), 9.03 (1H, s, NH), 9.16 (1H, s, NH).

HPLC: retention time 3.76 min.

Experiment 32

Preparation and Analysis of 116141

{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(cyclohexyl)carboxamide
[Protocol B] – cyclohexylamine

colourless solid, m.p. 155.5-156.3°C (EtOAc/hexane).

MS (ES+): m/z (%) = 379 (M+H ^{81}Br , 93), 377 (M+H ^{79}Br , 100).

$^1\text{H-NMR}$ (DMSO d_6): δ = 1.07-1.34 (5H, m, 5xCH), 1.52 (1H, m, CH), 1.63 (2H, m, 2xCH), 1.76 (2H, m, 2xCH), 3.48 (1H, m, NCH), 3.74 (3H, s, CH₃), 6.15 (1H, d, J=7.8, ArH), 6.98 (1H, d, J=7.5, ArH), 7.32-7.43 (2H, m, ArH), 7.51 (1H, m, NH), 7.62 (1H, s, ArH), 8.50 (1H, s, NH).

HPLC: retention time 3.16 min [Method A].

TLC: retention factor 0.35 (50% EtOAc/hexane).

Experiment 33

Preparation and Analysis of 116143

{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(phenylmethyl)carboxamide
[Protocol B] – benzylamine

colourless solid, m.p. 144.5-146.2°C (EtOAc/hexane).

IR: \square_{max} = 1622, 1565, 1467, 1374, 1239, 973, 802, 752, 695 cm^{-1} .

MS (ES+): m/z (%) = 387 (M+H ^{81}Br , 89), 385 (M+H ^{79}Br , 100).

$^1\text{H-NMR}$ (CD₃OD): δ = 3.81 (3H, s, CH₃), 4.40 (2H, s, CH₂), 7.05 (1H, m, ArH), 7.19-7.51 (9H, m, ArH).

HPLC: retention time 3.06 min [Method A].a

Experiment 34

Preparation and Analysis of 116144

{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(2-fluorophenyl)carboxamide

[Protocol A] – 2-fluorophenyl isocyanate

colourless solid (DCM/hexane)

MS (ES⁺): m/z (%) = 391 (M+H ⁸¹Br, 100), 389 (M+H ⁷⁹Br, 90).

¹H-NMR (MeOH d₄): δ = 3.79 (3H, s, NCH₃), 7.00-7.11 (4H, m, ArH), 7.40-7.56 (3H, m, ArH), 7.61 (1H, m, ArH), 8.09 (1H, m, ArH).

HPLC: retention time 3.01 min.

Experiment 35

Preparation and Analysis of 116145

2-({[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}carbonylamino)benzamide

[Protocol B] – 2-aminobenzamide

colourless solid (EtOAc/hexane)

MS (ES⁺): m/z (%) = 399 (M+H -17 ⁸¹Br, 100), 397 (M+H - 17 ⁷⁹Br, 94).

¹H-NMR (DMSO d₆): δ = 3.79 (3H, s, NCH₃), 6.93-7.10 (2H, m, ArH), 7.45 (2H, t, J=7.8, ArH), 7.59-7.72 (5H, m, ArH), 8.22 (2H, m), 9.92 (1H, s, NH), 10.69 (1H, s, NH).

HPLC: retention time 2.88 min.

Experiment 36

Preparation and Analysis of 116147

{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(4-cyanophenyl)carboxamide

[Protocol B] – 4-aminobenzonitrile

colourless solid (EtOAc/hexane)

MS (ES⁺): m/z (%) = 398 (M+H ⁸¹Br, 100), 396 (M+H ⁷⁹Br, 96).

¹H-NMR (MeOH d₄): δ = 3.81 (3H, s, NCH₃), 7.12 (1H, m, ArH), 7.46-7.57 (3H, m, ArH), 7.62-7.69 (5H, m, ArH).

HPLC: retention time 3.12 min.

Experiment 37

Preparation and Analysis of AR116148

{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(2-cyanophenyl)carboxamide

[Protocol B] – 2-aminobenzonitrile

colourless solid (EtOAc/hexane)

MS (ES+): m/z (%) = 398 (M+H ^{81}Br , 95), 396 (M+H ^{79}Br , 100).

$^1\text{H-NMR}$ (CDCl_3): δ = 3.79 (3H, s, CH_3), 7.13-7.28 (2H, m, ArH), 7.49 (1H, t, $J=7.8$, ArH), 7.57 (1H, m, ArH), 7.62 (1H, m, ArH), 7.65-7.71 (2H, m, ArH), 7.78 (1H, m, ArH), 8.07 (1H, d, $J=8.6$, ArH), 8.83 (1H, s, NH), 9.62 (1H, s, NH).

HPLC: retention time 3.05 min [Method A].

Experiment 38

Preparation and Analysis of 116182

{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(4-fluorophenylmethyl)carboxamide

[Protocol B] – 4-fluorobenzylamine

colourless solid, m.p. 185.5-186.6°C (EtOAc/hexane).

MS (ES+): m/z (%) = 405 (M+H ^{81}Br , 97), 403 (M+H ^{79}Br , 100).

$^1\text{H-NMR}$ ($\text{DMSO } d_6$): δ = 3.75 (3H, s, CH_3), 4.28 (2H, d, $J=6.0$, CH_2), 6.73 (1H, t, $J=5.9$, NH), 7.01 (1H, d, $J=7.5$, ArH), 7.10-7.18 (2H, m, ArH), 7.27-7.41 (4H, m, ArH), 7.56 (1H, s, ArH), 7.62 (1H, s, ArH), 8.82 (1H, s, NH).

HPLC: retention time 3.10 min [Method A].

TLC: retention factor 0.25 (50% EtOAc/hexane).

Experiment 39

Preparation and Analysis of 116183

{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(3,4-dimethoxyphenylmethyl)carboxamide

[Protocol B] – 3,4-dimethoxybenzylamine

colourless solid, m.p. 174.9-175.5°C (EtOAc/hexane).

MS (CI+): m/z (%) = 447 (M+H ^{81}Br , 100), 445 (M+H ^{79}Br , 92).

$^1\text{H-NMR}$ ($\text{DMSO } d_6$): δ = 3.71 (3H, s, CH_3), 3.73 (3H, s, CH_3), 3.76 (3H, s, CH_3), 4.22 (2H, d, $J=5.8$, CH_2), 6.62 (1H, t, $J=5.7$, NH), 6.80 (1H, m, ArH), 6.89 (2H, m, ArH), 6.98 (1H, m, ArH), 7.36-7.51 (3H, m, ArH), 7.63 (1H, s, ArH), 8.76 (1H, s, NH).

HPLC: retention time 2.86 min [Method A].

TLC: retention factor 0.20 (50% EtOAc/hexane).

Experiment 40

Preparation and Analysis of 116184

{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(3,4,5-trimethoxyphenylmethyl)carboxamide
[Protocol B] – 3,4,5-trimethoxybenzylamine

5 colourless solid (EtOAc/hexane).

MS (CI⁺): m/z (%) = 477 (M+H ⁸¹Br, 100), 475 (M+H ⁷⁹Br, 95).

¹H-NMR (DMSO d_6): δ = 3.63 (3H, s, OCH₃), 3.75 (9H, s, 3xCH₃), 4.21 (1H, d, J=5.9, CH₂), 6.61 (2H, s, ArH), 6.65 (1H, t, J=5.9, NH), 6.99 (1H, m, ArH), 7.40 (1H, t, J=7.7, ArH), 7.45 (1H, m, ArH), 7.56 (1H, m, ArH), 7.64 (1H, s, ArH), 8.77 (1H, s, NH).

10 HPLC: retention time 5.91 min [Method B].

TLC: retention factor 0.50 (50% EtOAc/hexane).

Experiment 41

Preparation and Analysis of 116185

15 {[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(2-methylphenylmethyl)carboxamide
[Protocol B] – 2-methylbenzylamine

colourless solid (EtOAc/hexane).

MS (CI⁺): m/z (%) = 401 (M+H ⁸¹Br, 96), 399 (M+H ⁷⁹Br, 100).

¹H-NMR (DMSO d_6): δ = 2.28 (3H, s, CH₃), 3.76 (3H, s, NCH₃), 4.28 (1H, d, J=5.8, CH₂), 6.60 (1H, t, J=5.8, NH), 7.01 (1H, m, ArH), 7.15 (3H, m, ArH), 7.24 (1H, m, ArH), 7.38-7.50 (2H, m, ArH), 7.57 (1H, m, ArH), 7.65 (1H, s, ArH), 8.77 (1H, s, NH).

20 HPLC: retention time 2.74 min [Method A].

TLC: retention factor 0.20 (50% EtOAc/hexane).

Experiment 42

Preparation and Analysis of 116189

25 {[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-(4-methoxyphenylmethyl)carboxamide
[Protocol B] – 4-methoxybenzylamine

colourless solid (EtOAc/hexane).

30 MS (CI⁺): m/z (%) = 417 (M+H ⁸¹Br, 94), 415 (M+H ⁷⁹Br, 100).

¹H-NMR (DMSO d_6): δ = 3.72 (3H, s, CH₃), 3.77 (3H, s, NCH₃), 4.22 (1H, d, J=5.9, CH₂), 6.62 (1H, t, J=5.9, NH), 6.90 (2H, d, J=8.8, ArH), 7.00 (1H, m, ArH), 7.23 (2H, d,

J=8.8, ArH), 7.39 (1H, t, J=7.8, ArH), 7.43 (1H, m, ArH), 7.56 (1H, m, ArH), 7.64 (1H, s, ArH), 8.73 (1H, s, NH).

HPLC: retention time 6.41 min [Method B].

TLC: retention factor 0.25 (50% EtOAc/hexane).

5

Experiment 43

Preparation and Analysis of 116194

{[3-(4-bromo-1-methylpyrazol-3-yl)phenyl]amino}-N-[2-(4-methoxy)phenylethyl]carboxamide
[Protocol B] – 2-(4-methoxyphenyl)ethylamine

10 colourless solid (EtOAc/hexane).

MS (ES⁺): *m/z* (%) = 431 (M+H ⁸¹Br, 95), 429 (M+H ⁷⁹Br, 100).

¹H-NMR (DMSO *d*₆): δ = 2.68 (2H, t, J=7.1, CH₂), 3.31 (2H, m, CH₂), 3.71 (3H, s, CH₃), 3.77 (3H, s, CH₃), 6.16 (1H, t, J=5.8, NH), 6.87 (2H, d, J=8.6, ArH), 6.99 (1H, dt, J=1.4, 7.3, ArH), 7.16 (2H, d, J=8.6, ArH), 7.33-7.48 (2H, m, ArH), 7.52 (1H, m, ArH),
15 7.63 (1H, s, ArH), 8.71 (1H, s, NH).

HPLC: retention time 6.62 min [Method B].

An important point that can be derived from the foregoing data is that by using a constitutively activated form of the receptor in the direct identification of candidate
20 compounds, the selectivity of the compounds is exceptional: as those in the art appreciate, the homology between the human 5HT_{2A} and 5HT_{2C} receptors is about 95%, and even with such homology, certain of the directly identified compounds evidence a 4-order-of-magnitude (10,000-fold) selectivity separation (116100). This is important for pharmaceutical compositions in that such selectivity can help to reduce side-effects associated with interaction
25 of a drug with a non-target receptor.

Different embodiments of the invention will consist of different constitutively activated receptors, different expression systems, different assays, and different compounds. Those skilled in the art will understand which receptors to use with which expression systems and assay methods. All are considered within the scope of the teaching of this invention. In
30 addition, those skilled in the art will recognize that various modifications, additions, substitutions, and variations to the illustrative examples set forth herein can be made without departing from the spirit of the invention and are, therefore, considered within the scope of the invention.

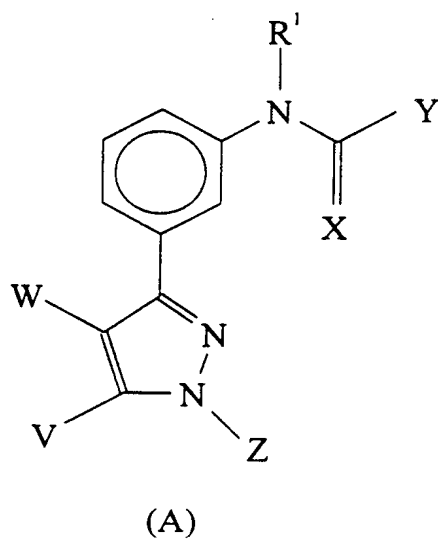
CLAIMS

We claim:

1. A cDNA encoding a constitutively active, non-endogenous version, of a human
5 5HT_{2C} serotonin receptor comprising SEQ. ID NO. 28.
2. A constitutively active non-endogenous human 5HT_{2C} serotonin receptor encoded
by the cDNA of SEQ ID NO. 28 comprising SEQ ID NO. 29.
3. A cDNA encoding a constitutively active, non-endogenous version, of a human
5HT_{2A} serotonin receptor comprising SEQ. ID NO. 30.
- 10 4. A constitutively active non-endogenous human 5HT_{2A} serotonin receptor encoded
by the cDNA of SEQ ID NO. 30 comprising SEQ ID NO. 31.
5. A cDNA encoding a constitutively active, non-endogenous version, of a human
5HT_{2A} serotonin receptor comprising SEQ. ID NO. 32.
6. A constitutively active non-endogenous human 5HT_{2A} serotonin receptor encoded
15 by the cDNA of SEQ ID NO. 32 comprising SEQ ID NO. 33.
7. A method for identifying whether a candidate compound is an inverse agonist to a
non-endogenous human 5HT₂ serotonin receptor comprising the steps of:
 - a. contacting the candidate compound with a non-endogenous human 5HT₂
serotonin receptor ; and
 - 20 b. determining, by measurement of a second messenger response whether said
compound is an inverse agonist.
8. The method of claim 7 in which the non-endogenous human 5HT₂ serotonin
receptor comprises SEQ ID NO. 29.
9. The method of claim 7 in which the non-endogenous human 5HT₂ serotonin
25 receptor comprises SEQ ID NO. 31.
10. The method of claim 7 in which the non-endogenous human 5HT₂ serotonin
receptor comprises SEQ ID NO. 33.
11. An inverse agonist identified by the method of claim 7.
12. A reagent for screening compounds to determine whether the compounds are inverse
30 agonists at human 5HT₂ serotonin receptors comprising a membrane fraction from
mammalian cells transfected with and expressing a cDNA encoding for a
constitutively active, non-endogenous version, of a human 5HT₂ serotonin receptor

in which the constitutively active non-endogenous human 5HT₂ receptor is expressed on the cell surface.

13. A reagent for screening compounds to determine whether the compounds are inverse agonists at human 5HT₂ serotonin receptors comprising mammalian cells which produce a second messenger response, transfected with and expressing a cDNA encoding for a constitutively active, non-endogenous version, of a human 5HT₂ serotonin receptor in which the constitutively active non-endogenous human 5HT₂ receptor is expressed on the cell surface.
14. A method for modulating by inverse agonism the activity of a human 5HT_{2A} serotonin receptor by contacting the receptor with a compound of formula:



Wherein:

- W is lower alkyl (C₁₋₆), or halogen;
 V is lower alkyl (C₁₋₆), or halogen;
 X is either Oxygen or Sulfur;
 Y is NR²R³, or (CH₂)_mR⁴, or O(CH₂)_nR⁴;
 Z is lower alkyl (C₁₋₆);
 m = 0 - 4
 n = 0 - 4
 R¹ is H or lower alkyl (C₁₋₄);
 R² is H or lower alkyl (C₁₋₄);

R^3 and R^4 are independently a C_{1-6} alkyl, or C_{2-6} alkenyl, or cycloalkyl, or aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from CF_3 , CCl_3 , Me, NO_2 , OH, OMe, OEt, $CONR^5R^6$, NR^5R^6 , OCF_3 , SMe, $COOR^7$, $SO_2NR^5R^6$, SO_3R^7 , COMe, COEt, CO-lower alkyl, SCF_3CN , C_{2-6} alkenyl, H, halogens, C_{1-4} alkoxy, C_{3-6} cycloalkyl, C_{1-6} alkyl, aryl, and aryloxy wherein each of the C_{3-6} cycloalkyl, C_{1-6} alkyl, aryl, or aryloxy groups may be further optionally substituted by up to four substituents in any position independently selected from CF_3 , CCl_3 , Me, NO_2 , OH, OMe, OEt, $CONR^5R^6$, NR^5R^6 , $NHCOCH_3$, OCF_3 , SMe, $COOR^7$, SO_3R^7 , $SO_2NR^5R^6$, COMe, COEt, CO-lower alkyl, SCF_3 , CN, C_{2-6} alkenyl, H, halogens, C_{1-4} alkoxy, C_{3-6} cycloalkyl, C_{1-6} alkyl, and aryl;

R^5 and R^6 are independently a H, or C_{1-6} alkyl, or C_{2-6} alkenyl, or cycloalkyl, or aryl, or CH_2 aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from CF_3 , CCl_3 , Me, NO_2 , OH, OMe, OEt, $CONR^7R^8$, NR^7R^8 , $NHCOCH_3$, OCF_3 , SMe, $COOR^9$, SO_3R^7 , $SO_2NR^7R^8$, COMe, COEt, CO-lower alkyl, SCF_3 , CN, C_{2-6} alkenyl, H, halogens, C_{1-4} alkoxy, C_{3-6} cycloalkyl, C_{1-6} alkyl, and aryl wherein each of the C_{3-6} cycloalkyl, C_{1-6} alkyl, or aryl groups may be further optionally substituted by up to four substituents in any position independently selected from CF_3 , CCl_3 , Me, NO_2 , OH, OMe, OEt, $CONR^8R^9$, NR^8R^9 , $NHCOCH_3$, OCF_3 , SMe, $COOR^7$, $SO_2NR^8R^9$, SO_3R^7 , COMe, COEt, CO-lower alkyl, SCF_3 , CN, C_{2-6} alkenyl, H, halogens, C_{1-4} alkoxy, C_{3-6} cycloalkyl, C_{1-6} alkyl, and aryl,

or R^5 and R^6 may form part of a 5, 6 or 7 membered cyclic structure which may be either saturated or unsaturated and that may contain up to four heteroatoms selected from O, N or S and said cyclic structure may be optionally substituted by up to four substituents in any position independently selected from CF_3 , CCl_3 , Me, NO_2 , OH, OMe, OEt, OCF_3 , SMe, $COOR^7$, $SO_2NR^8R^9$, SO_3R^7 , $NHCOCH_3$, COEt, COMe, or halogen;

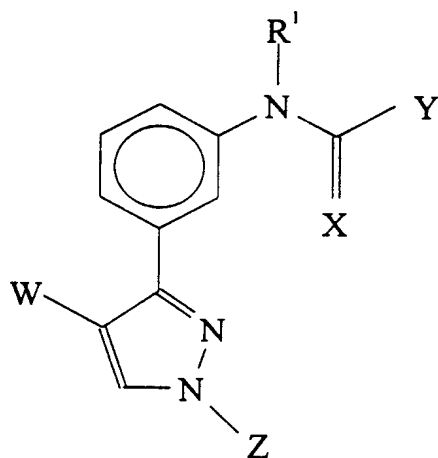
R^7 may be independently selected from H or C_{1-6} alkyl;

R^8 and R^9 are independently a H, or C_{1-6} alkyl, or C_{2-6} alkenyl, or cycloalkyl, or aryl, or CH_2 aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from

halogen, CF₃, OCF₃, OEt, CCl₃, Me, NO₂, OH, OMe, SMe, COMe, CN, COOR⁷, SO₃R⁷, COEt, NHCOCH₃, or aryl;

an aryl moiety can be a 5 or 6 membered aromatic heterocyclic ring (containing up to 4 hetero atoms independently selected from N, O, or S) or a 6 membered aromatic non-heterocyclic ring or a polycycle;

15. A method for modulating by inverse agonism the activity of a human 5HT_{2A} serotonin receptor by contacting the receptor with a compound of formula:



(B)

Wherein:

W is Me, or Et, or halogen;

X is either Oxygen or Sulfur;

Y is NR²R³, or (CH₂)_mR⁴, or O(CH₂)_nR⁴;

Z is lower alkyl (C₁₋₆);

m = 0 - 4

n = 0 - 4

R¹ is H or lower alkyl (C₁₋₄);

R² is H or lower alkyl (C₁₋₄);

R³ and R⁴ are independently a C₁₋₆ alkyl, or C₂₋₆ alkenyl, or cycloalkyl, or aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁵R⁶, NR⁵R⁶, OCF₃, SMe, COOR⁷, SO₂NR⁵R⁶, SO₃R⁷, COMe, COEt, CO-lower alkyl, SCF₃CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆

cycloalkyl, C₁₋₆ alkyl, aryl, and aryloxy wherein each of the C₃₋₆ cycloalkyl, C₁₋₆ alkyl, aryl, or aryloxy groups may be further optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁵R⁶, NR⁵R⁶, NHCOCH₃, OCF₃, SMe, COOR⁷, SO₃R⁷, SO₂NR⁵R⁶, COMe, COEt, CO-lower alkyl, SCF₃, CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, and aryl;

R⁵ and R⁶ are independently a H, or C₁₋₆ alkyl, or C₂₋₆ alkenyl, or cycloalkyl, or aryl, or CH₂ aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁷R⁸, NR⁷R⁸, NHCOCH₃, OCF₃, SMe, COOR⁹, SO₃R⁷, SO₂NR⁷R⁸, COMe, COEt, CO-lower alkyl, SCF₃, CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, and aryl wherein each of the C₃₋₆ cycloalkyl, C₁₋₆ alkyl, or aryl groups may be further optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁸R⁹, NR⁸R⁹, NHCOCH₃, OCF₃, SMe, COOR⁷, SO₂NR⁸R⁹, SO₃R⁷, COMe, COEt, CO-lower alkyl, SCF₃, CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, and aryl,

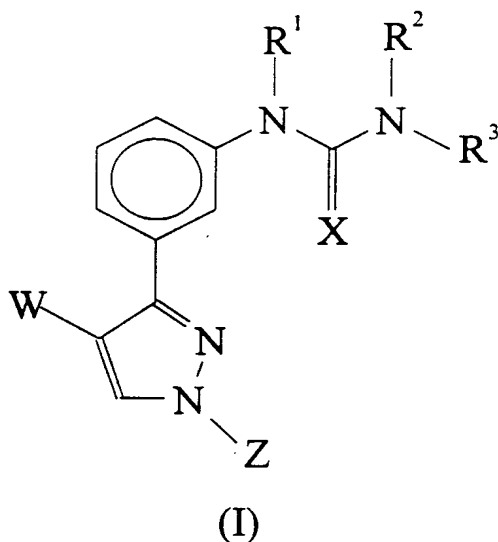
or R⁵ and R⁶ may form part of a 5, 6 or 7 membered cyclic structure which may be either saturated or unsaturated and that may contain up to four heteroatoms selected from O, N or S and said cyclic structure may be optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, OCF₃, SMe, COOR⁷, SO₂NR⁸R⁹, SO₃R⁷, NHCOCH₃, COEt, COMe, or halogen;

R⁷ may be independently selected from H or C₁₋₆ alkyl;

R⁸ and R⁹ are independently a H, or C₁₋₆ alkyl, or C₂₋₆ alkenyl, or cycloalkyl, or aryl, or CH₂aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from halogen, CF₃, OCF₃, OEt, CCl₃, Me, NO₂, OH, OMe, SMe, COMe, CN, COOR⁷, SO₃R⁷, COEt, NHCOCH₃, or aryl;

an aryl moiety can be a 5 or 6 membered aromatic heterocyclic ring (containing up to 4 hetero atoms independently selected from N, O, or S) or a 6 membered aromatic non-heterocyclic ring or a polycycle.

16. A method for modulating by inverse agonism the activity of a human 5HT_{2A} serotonin receptor by contacting the receptor with a compound of formula:



Wherein:

Preferably R¹ and R² are H.

Preferably W is Br.

Preferably X is O.

Preferably Z is Me.

R³ is C₁₋₆ alkyl, or C₂₋₆ alkenyl, or cycloalkyl, or aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁵R⁶, NR⁵R⁶, OCF₃, SMe, COOR⁷, SO₂NR⁵R⁶, SO₃R⁷, COMe, COEt, CO-lower alkyl, SCF₃CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, aryl, and aryloxy wherein each of the C₃₋₆ cycloalkyl, C₁₋₆ alkyl, aryl, or aryloxy groups may be further optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁵R⁶, NR⁵R⁶, NHCOCH₃, OCF₃, SMe, COOR⁷, SO₃R⁷, SO₂NR⁵R⁶, COMe, COEt, CO-lower alkyl, SCF₃, CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, and aryl;

R⁵ and R⁶ are independently a H, or C₁₋₆ alkyl, or C₂₋₆ alkenyl, or cycloalkyl, or aryl, or CH₂ aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁷R⁸, NR⁷R⁸, NHCOCH₃, OCF₃, SMe.

COOR⁹, SO₃R⁷, SO₂NR⁷R⁸, COMe, COEt, CO-lower alkyl, SCF₃, CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, and aryl wherein each of the C₃₋₆ cycloalkyl, C₁₋₆ alkyl, or aryl groups may be further optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁸R⁹, NR⁸R⁹, NHCOCH₃, OCF₃, SMe, COOR⁷, SO₂NR⁸R⁹, SO₃R⁷, COMe, COEt, CO-lower alkyl, SCF₃, CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, and aryl,

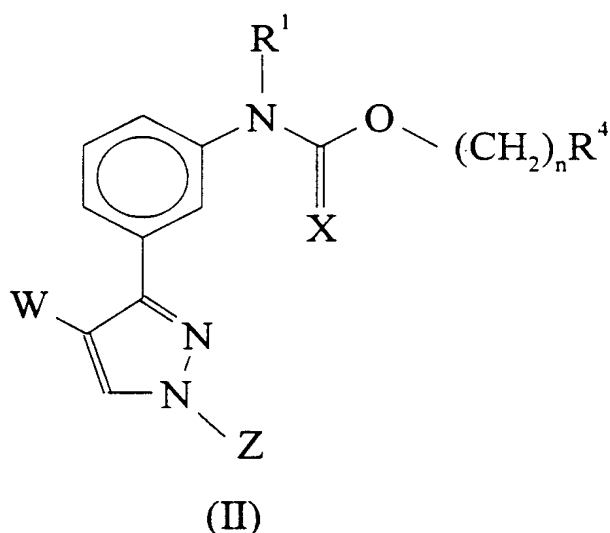
or R⁵ and R⁶ may form part of a 5, 6 or 7 membered cyclic structure which may be either saturated or unsaturated and that may contain up to four heteroatoms selected from O, N or S and said cyclic structure may be optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, OCF₃, SMe, COOR⁷, SO₂NR⁸R⁹, SO₃R⁷, NHCOCH₃, COEt, COMe, or halogen;

R⁷ may be independently selected from H or C₁₋₆ alkyl;

R⁸ and R⁹ are independently a H, or C₁₋₆ alkyl, or C₂₋₆ alkenyl, or cycloalkyl, or aryl, or CH₂aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from halogen, CF₃, OCF₃, OEt, CCl₃, Me, NO₂, OH, OMe, SMe, COMe, CN, COOR⁷, SO₃R⁷, COEt, NHCOCH₃, or aryl;

an aryl moiety can be a 5 or 6 membered aromatic heterocyclic ring (containing up to 4 hetero atoms independently selected from N, O, or S) or a 6 membered aromatic non-heterocyclic ring or a polycycle.

17. A method for modulating by inverse agonism the activity of a human 5HT_{2A} serotonin receptor by contacting the receptor with a compound of formula:



Wherein:

Preferably R¹ is H.

Preferably W is Br.

5 Preferably X is O.

Preferably Z is Me.

n = 0 - 4

R⁴ is C₁₋₆ alkyl, or C₂₋₆ alkenyl, or cycloalkyl, or aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁵R⁶, NR⁵R⁶, OCF₃, SMe, COOR⁷, SO₂NR⁵R⁶, SO₃R⁷, COMe, COEt, CO-lower alkyl, SCF₃CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, aryl, and aryloxy wherein each of the C₃₋₆ cycloalkyl, C₁₋₆ alkyl, aryl, or aryloxy groups may be further optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁵R⁶, NR⁵R⁶, NHCOCH₃, OCF₃, SMe, COOR⁷, SO₃R⁷, SO₂NR⁵R⁶, COMe, COEt, CO-lower alkyl, SCF₃, CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, and aryl;

R⁵ and R⁶ are independently a H, or C₁₋₆ alkyl, or C₂₋₆ alkenyl, or cycloalkyl, or aryl, or CH₂ aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁷R⁸, NR⁷R⁸, NHCOCH₃, OCF₃, SMe, COOR⁹, SO₃R⁷, SO₂NR⁷R⁸, COMe, COEt, CO-lower alkyl, SCF₃, CN, C₂₋₆ alkenyl.

H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, and aryl wherein each of the C₃₋₆ cycloalkyl, C₁₋₆ alkyl, or aryl groups may be further optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁸R⁹, NR⁸R⁹, NHCOCH₃, OCF₃, SMe, COOR⁷, SO₂NR⁸R⁹, SO₃R⁷, COMe, COEt, CO-lower alkyl, SCF₃, CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, and aryl,

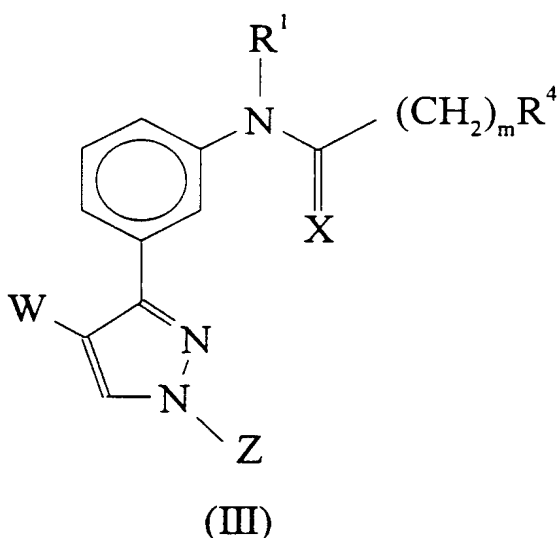
or R⁵ and R⁶ may form part of a 5, 6 or 7 membered cyclic structure which may be either saturated or unsaturated and that may contain up to four heteroatoms selected from O, N or S and said cyclic structure may be optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, OCF₃, SMe, COOR⁷, SO₂NR⁸R⁹, SO₃R⁷, NHCOCH₃, COEt, COMe, or halogen;

R⁷ may be independently selected from H or C₁₋₆ alkyl;

R⁸ and R⁹ are independently a H, or C₁₋₆ alkyl, or C₂₋₆ alkenyl, or cycloalkyl, or aryl, or CH₂aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from halogen, CF₃, OCF₃, OEt, CCl₃, Me, NO₂, OH, OMe, SMe, COMe, CN, COOR⁷, SO₃R⁷, COEt, NHCOCH₃, or aryl;

an aryl moiety can be a 5 or 6 membered aromatic heterocyclic ring (containing up to 4 hetero atoms independently selected from N, O, or S) or a 6 membered aromatic non-heterocyclic ring or a polycycle.

18. A method for modulating by inverse agonism the activity of a human 5HT_{2A} serotonin receptor by contacting the receptor with a compound of formula:



Wherein:

Preferably W is Br.

Preferably X is O.

5 Preferably Z is Me.

Preferably R¹ is H.

m = 0 - 4

R⁴ is C₁₋₆ alkyl, or C₂₋₆ alkenyl, or cycloalkyl, or aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁵R⁶, NR⁵R⁶, OCF₃, SMe, COOR⁷, SO₂NR⁵R⁶, SO₃R⁷, COMe, COEt, CO-lower alkyl, SCF₃CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, aryl, and aryloxy wherein each of the C₃₋₆ cycloalkyl, C₁₋₆ alkyl, aryl, or aryloxy groups may be further optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁵R⁶, NR⁵R⁶, NHCOCH₃, OCF₃, SMe, COOR⁷, SO₃R⁷, SO₂NR⁵R⁶, COMe, COEt, CO-lower alkyl, SCF₃, CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, and aryl;

R⁵ and R⁶ are independently a H, or C₁₋₆ alkyl, or C₂₋₆ alkenyl, or cycloalkyl, or aryl, or CH₂ aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁷R⁸, NR⁷R⁸, NHCOCH₃, OCF₃, SMe, COOR⁹, SO₃R⁷, SO₂NR⁷R⁸, COMe, COEt, CO-lower alkyl, SCF₃, CN, C₂₋₆ alkenyl.

H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, and aryl wherein each of the C₃₋₆ cycloalkyl, C₁₋₆ alkyl, or aryl groups may be further optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁸R⁹, NR⁸R⁹, NHCOCH₃, OCF₃, SMe, COOR⁷, SO₂NR⁸R⁹, SO₃R⁷, COMe, COEt, CO-lower alkyl, SCF₃, CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, and aryl,

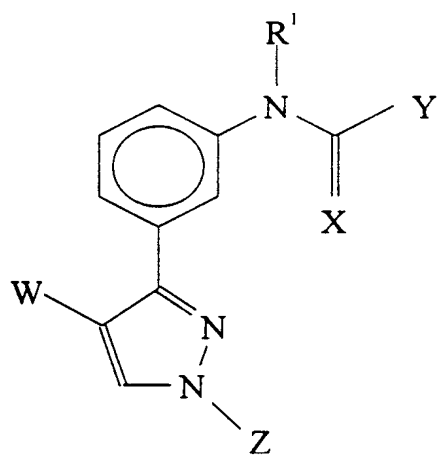
or R⁵ and R⁶ may form part of a 5, 6 or 7 membered cyclic structure which may be either saturated or unsaturated and that may contain up to four heteroatoms selected from O, N or S and said cyclic structure may be optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, OCF₃, SMe, COOR⁷, SO₂NR⁸R⁹, SO₃R⁷, NHCOCH₃, COEt, COMe, or halogen;

R⁷ may be independently selected from H or C₁₋₆ alkyl;

R⁸ and R⁹ are independently a H, or C₁₋₆ alkyl, or C₂₋₆ alkenyl, or cycloalkyl, or aryl, or CH₂aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from halogen, CF₃, OCF₃, OEt, CCl₃, Me, NO₂, OH, OMe, SMe, COMe, CN, COOR⁷, SO₃R⁷, COEt, NHCOCH₃, or aryl;

an aryl moiety can be a 5 or 6 membered aromatic heterocyclic ring (containing up to 4 hetero atoms independently selected from N, O, or S) or a 6 membered aromatic non-heterocyclic ring or a polycycle.

19. A compound of formula (C)



(C)

Wherein:

W is Me, or Et, or halogen;

X is either Oxygen or Sulfur;

Y is NR^2R^3 , or $(\text{CH}_2)_m\text{R}^4$, or $\text{O}(\text{CH}_2)_n\text{R}^4$;

Z is lower alkyl (C_{1-6});

$m = 0 - 4$;

$n = 0 - 4$;

R^1 is H or lower alkyl (C_{1-4});

R^2 is H or lower alkyl (C_{1-4});

R^3 is a C_{1-6} alkyl, or C_{2-6} alkenyl, or cycloalkyl, or $(\text{CH}_2)_k$ aryl group ($k = 1 - 4$), preferably $k = 1$, and each said group may be optionally substituted by up to four substituents in any position independently selected from CF_3 , CCl_3 , Me, NO_2 , OH, OMe, OEt, CONR^5R^6 , NR^5R^6 , OCF_3 , SMe, COOR^7 , $\text{SO}_2\text{NR}^5\text{R}^6$, SO_3R^7 , COMe, COEt, CO-lower alkyl, SCF_3CN , C_{2-6} alkenyl, H, halogens, C_{1-4} alkoxy, C_{3-6} cycloalkyl, C_{1-6} alkyl, aryl, and aryloxy wherein each of the C_{3-6} cycloalkyl, C_{1-6} alkyl, aryl, or aryloxy groups may be further optionally substituted by up to four substituents in any position independently selected from CF_3 , CCl_3 , Me, NO_2 , OH, OMe, OEt, CONR^5R^6 , NR^5R^6 , NHCOCH_3 , OCF_3 , SMe, COOR^7 , SO_3R^7 .

SO₂NR⁵R⁶, COMe, COEt, CO-lower alkyl, SCF₃, CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, and aryl;

R⁴ is a C₁₋₆ alkyl, or C₂₋₆ alkenyl, or cycloalkyl, or aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁵R⁶, NR⁵R⁶, OCF₃, SMe, COOR⁷, SO₂NR⁵R⁶, SO₃R⁷, COMe, COEt, CO-lower alkyl, SCF₃CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, aryl, and aryloxy wherein each of the C₃₋₆ cycloalkyl, C₁₋₆ alkyl, aryl, or aryloxy groups may be further optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁵R⁶, NR⁵R⁶, NHCOCH₃, OCF₃, SMe, COOR⁷, SO₃R⁷, SO₂NR⁵R⁶, COMe, COEt, CO-lower alkyl, SCF₃, CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, and aryl;

R⁵ and R⁶ are independently a H, or C₁₋₆ alkyl, or C₂₋₆ alkenyl, or cycloalkyl, or aryl, or CH₂ aryl group and each said group may be optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁷R⁸, NR⁷R⁸, NHCOCH₃, OCF₃, SMe, COOR⁹, SO₃R⁷, SO₂NR⁷R⁸, COMe, COEt, CO-lower alkyl, SCF₃, CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, and aryl wherein each of the C₃₋₆ cycloalkyl, C₁₋₆ alkyl, or aryl groups may be further optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, CONR⁸R⁹, NR⁸R⁹, NHCOCH₃, OCF₃, SMe, COOR⁷, SO₂NR⁸R⁹, SO₃R⁷, COMe, COEt, CO-lower alkyl, SCF₃, CN, C₂₋₆ alkenyl, H, halogens, C₁₋₄ alkoxy, C₃₋₆ cycloalkyl, C₁₋₆ alkyl, and aryl,

or R⁵ and R⁶ may form part of a 5, 6 or 7 membered cyclic structure which may be either saturated or unsaturated and that may contain up to four heteroatoms selected from O, N or S and said cyclic structure may be optionally substituted by up to four substituents in any position independently selected from CF₃, CCl₃, Me, NO₂, OH, OMe, OEt, OCF₃, SMe, COOR⁷, SO₂NR⁸R⁹, SO₃R⁷, NHCOCH₃, COEt, COMe, or halogen;

R⁷ may be independently selected from H or C₁₋₆ alkyl;

R⁸ and R⁹ are independently a H, or C₁₋₆ alkyl, or C₂₋₆ alkenyl, or cycloalkyl, or aryl, or CH₂aryl group and each said group may be optionally

substituted by up to four substituents in any position independently selected from halogen, CF₃, OCF₃, OEt, CCl₃, Me, NO₂, OH, OMe, SMe, COMe, CN, COOR⁷, SO₃R⁷, COEt, NHCOCH₃, or aryl;

an aryl moiety can be a 5 or 6 membered aromatic heterocyclic ring (containing up to 4 hetero atoms independently selected from N, O, or S) or a 6 membered aromatic non-heterocyclic ring or a polycycle;

with the proviso that said compound is not:

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][methylamino]carboxamide, or

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][{(4-trifluoromethoxy)phenyl}amino]

carboxamide, or

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][2-chlorophenyl]carboxamide, or

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][2-chloro-3-pyridyl]carboxamide, or

N-[3-(4-bromo-1-methylpyrazol-3-yl)phenyl][trichloromethyl]carboxamide.

20. The use of a compound of claim 19 for the manufacture of a medicament.

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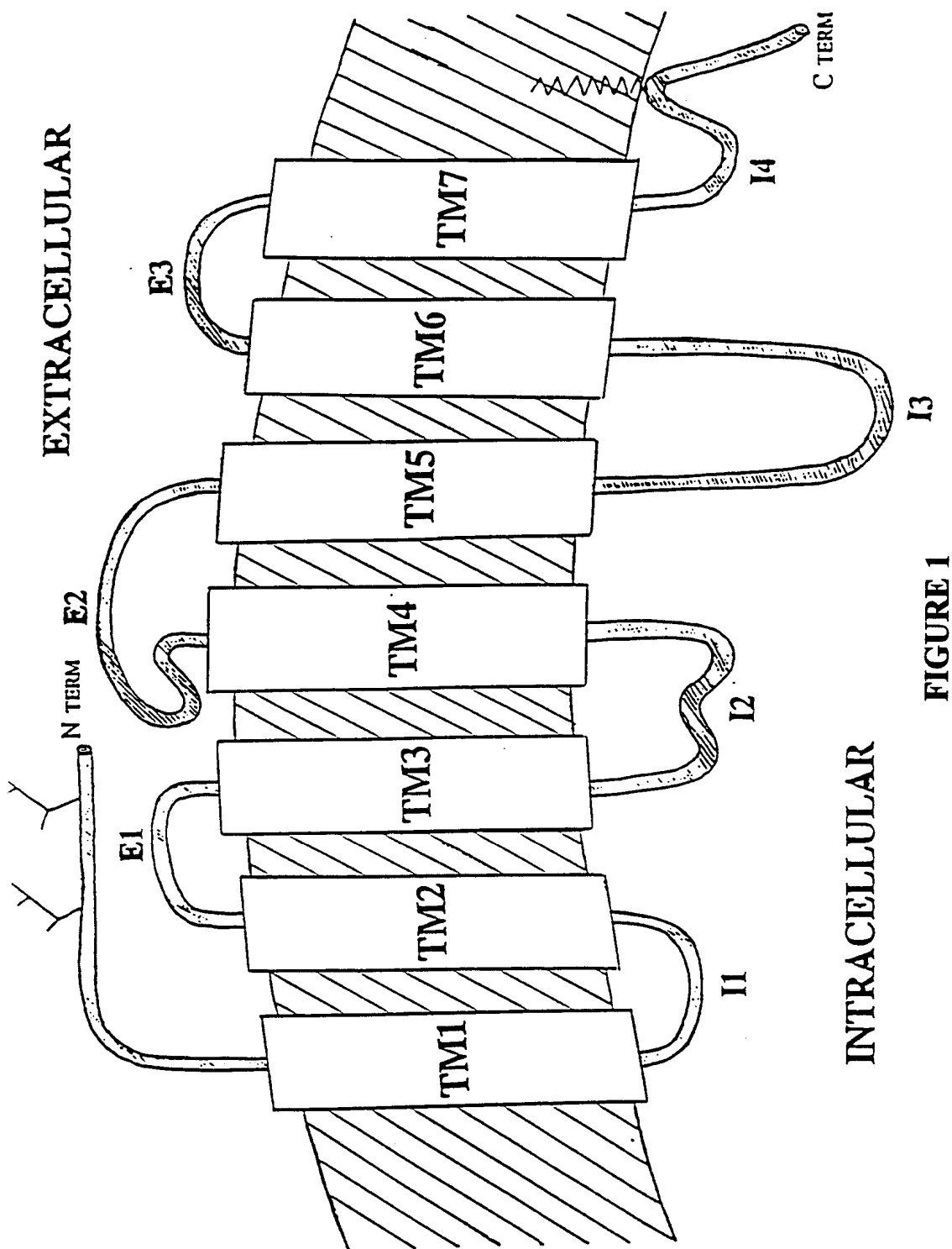


FIGURE 1

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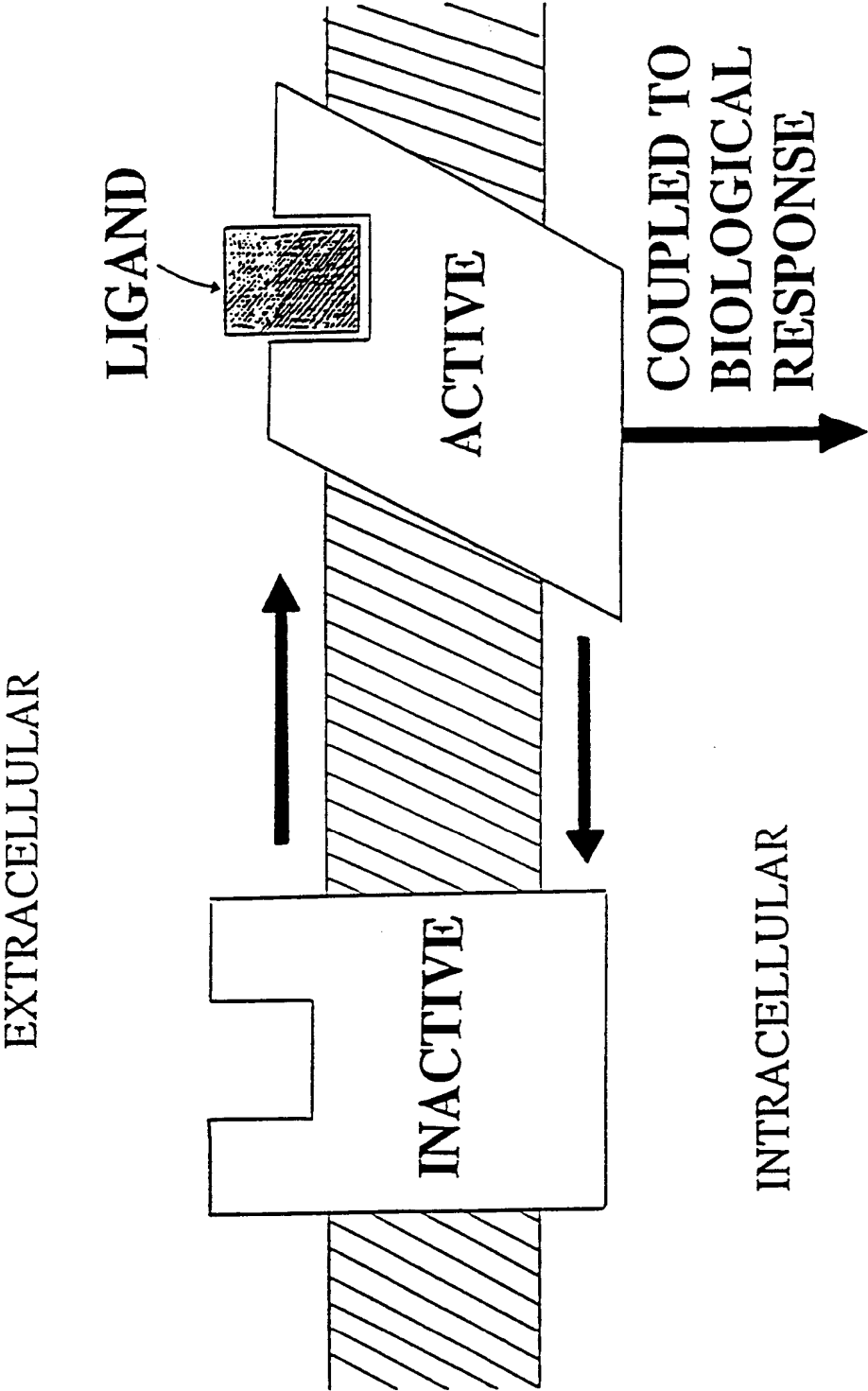


FIGURE 2

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FIGURE 3A

ATGGATATTCTTTGTGAAGAAAATACTTCTTTGAGCTCAACTACGAACTCCCTAATGCAATTA
AATGATGACAACAGGCTCTACAGTAATGACTTTAACTCCGGAGAAGCTAACACTTCTGATGCA
TTTAACTGGACAGTCGACTCTGAAAATCGAACCAACCTTTCCTGTGAAGGGTGCCTCTCACCG
TCGTGTCTCTCCTTACTTTCATCTCCAGGAAAAAACTGGTCTGCTTTACTGACAGCCGTAGTGA
TTATTCTAACTATTGCTGGAAACATACTCGTCATCATGGCAGTGTCCCTAGAGAAAAAGCTGC
AGAATGCCACCAACTATTTCTGTATGTCACTTGCCATAGCTGATATGCTGCTGGGTTTCCTTGT
CATGCCCGTGTCCATGTAAACCATCCTGTATGGGTACCGGTGGCCTCTGCCGAGCAAGCTTTGT
GCAGTCTGGATTTACCTGGACGTGCTCTTCTCCACGGCCTCCATCATGCACCTCTGCGCCATCT
CGCTGGACCGCTACGTGCGCATCCAGAATCCCATCCACCACAGCCGCTTCAACTCCAGAACTA
AGGCATTTCTGAAAATCATTGCTGTTTGGACCATATCAGTAGGTATATCCATGCCAATACCAG
TCTTTGGGCTACAGGACGATTCTGAAGGTCTTTAAGGAGGGGAGTTGCTTACTCGCCGATGATA
ACTTTGTCTGTATCGGCTCTTTTGTGTCATTTTTCATTCCCTTAACCATCATGGTGATCACCTAC
TTTCTAACTATCAAGTCACTCCAGAAAGAAGCTACTTTGTGTGTAAGTGATCTTGGCACACGG
GCCAAATTAGCTTCTTTTCTCAGCTTCTCCCTCAGAGTTCTTTGTCTTCAGAAAAGCTCTTCCAGC
GGTCGATCCATAGGGAGCCAGGGTCCTACACAGGCAGGAGGACTATGCAGTCCATCAGCAAT
GAGCAAAAGGCATGCAAGGTGCTGGGCATCGTCTTCTCCTGTTTGTGGTGATGTGGTGCCTT
TTCTTCATCACAAACATCATGGCCGTCATCTGCAAAGAGTCCTGCAATGAGGATGTCATTGGG
GCCCTGCTCAATGTGTTTGTGGATCGGTTATCTCTCTTCAGCAGTCAACCCACTAGTCTACA
CACTGTTCAACAAGACCTATAGGTGAGCCTTTTACGGTATATTCAGTGTGAGTACAAGGAAA
ACAAAAAACCATTGCAGTTAATTTTAGTGAACACAATACCGGCTTTGGCCTACAAGTCTAGCC
AACTTCAAATGGGACAAAAAAGAATTCAAAGCAAGATGCCAAGACAACAGATAATGACTGC
TCAATGGTTGCTCTAGGAAAGCAGTATTCTGAAGAGGCTTCTAAAGACAATAGCGACGGAGT
GAATGAAAAGGTGAGCTGTGTGTGA

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FIGURE 3B

MDILCEENTSLSSTTNSLMQLNDDNRLYSNDFNSGEANTSDAFNWTVDSENRTNLSCEGCLSPSCL
SLLHLQEKNWSALLTAVVHILTIAGNILVIMAVSLEKKLQNATNYFLMSLAIADMLLGFLVMPVSM
LTILYGYRWPLPSKLCVWVWYLDVLFSTASIMHLCAISLDRYVAIQNPIHHSRFSRNTKAFLKIAVW
TISVGISMPIPVFGLQDDSKVFKEGSCLLADDNFVLIGSFVSFFIPLTIMVITYFLTIKSLQKEATLCVS
DLGTRAKLASFSFLPQSSLSSEKLFQRSIHREPGSYTGRRTMQSISNEQKACKVLGIVFFLFVVMWC
PFFITNIMAVICKESCNEVDIGALLNVFVWIGYLSSAVNPLVYTLFNKTYRSAFSRYIQCQYKENKK
PLQLILVNTIPALAYKSSQLQMGQKKNSKQDAKTTDNDCSMVALGKQYSEEASKDNSDGVNEKV
SCV

FIGURE 4B

MVNLRNAVHSFLVHLIGLLVWQCDISVSPVAAIVTDIFNTSDGGRFKFPDGVQNWPAISIVIIIMTIGGN
ILVIMAVSMEKKLENATNYFLMSLAIADMLVGLLVMPLSLLAILYDYVWPLPRYLCPVWISLDVLFSTASI
MHLCAISLDRYVAIRNPIEHSRFSRNTKAIMKIAIVWALSIGVSVPIPVIGLRDEEKVFNNTTCVLNDPN
FVLIGSFVAFFIPLTIMVITYCLTIYVLRQALMLLHGHTTEPPGLSLDFLKCCKRNTAEEENSANPNQDQ
NARRRKKKERRPRGTMQAINNERKASKVLGIVFFVFLIMWCPFFITNILSVLCEKSCNQKLMKLLNVFVW
IGYVCSGINPLVYTLFNKIYRRAFSNYLRCNYKVEKKPPVRQIPRVAATALSGRELVNIYRHTNEPVIEK
ASDNEPGIEMQVENLELPVNPSSVVSERISSV

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FIGURE 4A

ATGGTGAACCTGAGGAATGCGGTGCATTTCCTTGTGCACCTAATTGGCCTATTGGTTTGGC
AATGTGATATTTCTGTGAGCCCAGTAGCAGCTATAGTAACTGACATTTTCAATACCTCCGATG
GTGGACGCTTCAAATTCCCAGACGGGGTACAAAAGTGGCCAGCACTTTCAATCGTCATCATAA
TAATCATGACAATAGGTGGCAACATCCTTGTGATCATGGCAGTAAGCATGGAAAAGAACTG
CACAATGCCACCAATTACTTCTTAATGTCCCTAGCCATTGCTGATATGCTAGTGGGACTACTTG
TCATGCCCCTGTCTCTCCTGGCAATCCTTTATGATTATGTCTGGCCACTACCTAGATATTTGTG
CCCCGTCTGGATTTCTTTAGATGTTTTATTTTCAACAGCGTCCATCATGCACCTCTGCGCTATAT
CGCTGGATCGGTATGTAGCAATACGTAATCCTATTGAGCATAGCCGTTTCAATTGCGGGACTA
AGGCCATCATGAAGATTGCTATTGTTTGGGCAATTTCTATAGGTGTATCAGTTCCTATCCCTGT
GATTGGACTGAGGGACGAAGAAAAGGTGTTCTGTGAACAACACGACGTGCGTGCTCAACGACC
CAAATTCGTTCTTATTGGGTCCTTCGTAGCTTTCTTCATACCGCTGACGATTATGGTGATTAC
GTATTGCCTGACCATCTACGTTCTGCGCCGACAAGCTTTGATGTTACTGCACGGCCACACCGA
GGAACCGCCTGGACTAAGTCTGGATTTCTGAAAGTGTGCAAGAGGAATACGGCCGAGGAAG
AGAACTCTGCAAACCTAACCAGACGACGACGCGGAAAGAAAGAAAGGAGAGACG
TCCTAGGGGCACCATGCAGGCTATCAACAATGAAAGAAAAGCTTCGAAAGTCCTTGGGATTG
TTTTCTTTGTGTTTCTGATCATGTGGTGCCCATTTTTTATTACCAATATTCTGTCTGTTCTTTGTG
AGAAGTCCTGTAACCAAAGCTCATGGAAAAGCTTCTGAATGTGTTTGTGTTGGATTGGCTATG
TTTGTTCAAGGAATCAATCCTCTGGTGTATACTCTGTTCAACAAAATTTACCGAAGGGCATTCTC
CAACTATTTGCGTTGCAATTATAAGGTAGAGAAAAAGCCTCCTGTCAGGCAGATTCCAAGAGT
TGCCGCCACTGCTTTGTCTGGGAGGGAGCTTAATGTTAACATTTATCGGCATACCAATGAACC
GGTGATCGAGAAAGCCAGTGACAATGAGCCCGGTATAGAGATGCAAGTTGAGAATTTAGAGT
TACCAGTAAATCCCTCCAGTGTGGTTAGCGAAAGGATTAGCAGTGTGTGA

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FIGURE 5A

ATGGTGAACCTGAGGAATGCGGTGCATTTCCTTGTGCACCTAATTGGCCTATTGGTTTGGCAAT
GTGATATTTCTGTGAGCCCAGTAGCAGCTATAGTAACTGACATTTTCAATACCTCCGATGGTGGACG
CTTCAAATTCCCAGACGGGGTACAAAAGTGGCCAGCACTTTCAATCGTCATCATAATAATCATGAC
AATAGGTGGCAACATCCTTGTGATCATGGCAGTAAGCATGGAAAAGAACTGCACAATGCCACCA
ATTACTTCTTAATGTCCCTAGCCATTGCTGATATGCTAGTGGGACTACTTGTATGCCCTGTCTCTC
CTGGCAATCCTTTATGATTATGTCTGGCCACTACCTAGATATTTGTGCCCCGTCTGGATTTCTTTAGA
TGTTTTATTTTCAACAGCGTCCATCATGCACCTCTGCGCTATATCGCTGGATCGGTATGTAGCAATA
CGTAATCCTATTGAGCATAGCCGTTTCAATTCGCGGACTAAGGCCATCATGAAGATTGCTATTGTTT
GGGCAATTTCTATAGGTGTATCAGTTCCTATCCCTGTGATTGGACTGAGGGACGAAGAAAAGGTGT
TCGTGAACAACACGACGTGCGTGCTCAACGACCCAAATTTGTTCTTATTGGGTCCTTCGTAGCTTT
CTTCATACCGCTGACGATTATGGTGATTACGTATTGCCTGACCATCTACGTTCTGCGCCGACAAGCT
TTGATGTTACTGCACGGCCACACCGAGGAACCGCCTGGACTAAGTCTGGATTTCTGAAGTGCTGC
AAGAGGAATACGGCCGAGGAAGAGAACTCTGAAAACCTAACCAAGACCAGAACGCACGCCGAA
GAAAGAAGAAGGAGAGACGTCCTAGGGGCACCATGCAGGCTATCAACAATGAAAGAAAAGCTAA
GAAAGTCCTTGGGATTGTTTTCTTTGTGTTTCTGATCATGTGGTGCCCATTTTTCATTACCAATATTC
TGTCTGTTCTTTGTGAGAAGTCCTGTAACCAAAAAGCTCATGGAAAAGCTTCTGAATGTGTTTGTG
GATTGGCTATGTTTGTTCAGGAATCAATCCTCTGGTGTATACTCTGTTCAACAAAATTTACCGAAGG
GCATTCTCCAATATTTGCGTTGCAATTATAAGGTAGAGAAAAAGCCTCCTGTCAGGCAGATTCCA
AGAGTTGCCGCCACTGCTTTGTCTGGGAGGGAGCTTAATGTTAACATTTATCGGCATACCAATGAA
CCGGTGATCGAGAAAGCCAGTGACAATGAGCCCGGTATAGAGATGCAAGTTGAGAATTTAGAGTT
ACCAGTAAATCCCTCCAGTGTGGTTAGCGAAAGGATTAGCAGTGTGTGA

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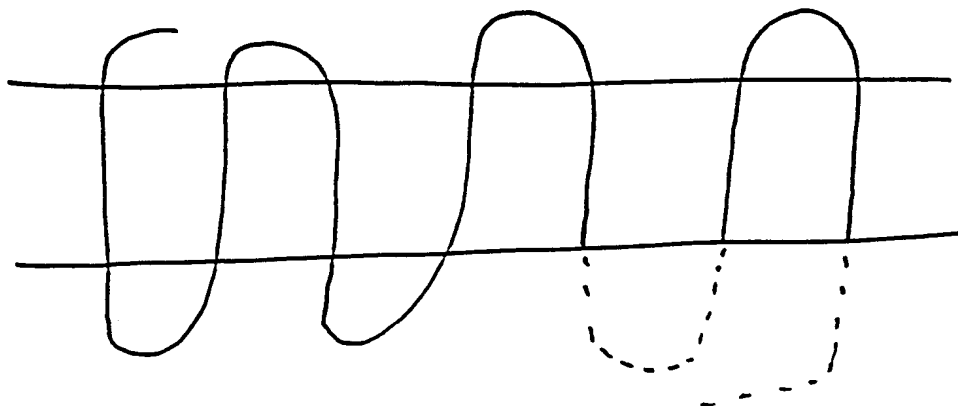
FIGURE 5B

MVNLRNAVHSFLVHLIGLLVWQCDISVSPVAAIVTDIFNTSDGGRFKFPDGVQNWPAISVIMMTI
 GGNILVIMAVSMEKKLHNATNYFLMSLAADMLVGLLVMPLSLLAILYDYVWPLPRYLCPVWISL
 DVLFSTASIMHLCAISLDTRYVAIRNPIEHSRFSRSTKAIMKIAIVWAISIGVSVPIPVIGLRDEEKVVFV
 NNTTCVLNDPNFVLIGSFVAFFIPLTIMVITYCLTIYVLRQALMLLHGHTTEPPGLSLDFLKCCCKRN
 TAEENSANPNQDQONARRRKKKERRPRGTMQAINNERKAKKVLGIVFFVFLIMWCPFFITNLSVL
 CEKSCNQKLMEKLLNVFVWIGYVCSGINPLVYTLFNKIYRRAFSNYLRCNYKVEKKPPVRQIPRV
 AATALSGRELNVNIYRHTNEPVIEKASDNEPGIEMQVENLELPVNPSSVVSERISSV.

FIGURE 6B

MDILCEENTSLSSTTNSLMQLNDDNRLYSNDFNSGEANTSDAFNWTVDSENRTNLSCEGCLSPSCL
 SLLHLQEKNEWSALLTAVVILTIAGNILVIMAVSLEKKLQNATNYFLMSLAADMLLGFLVMPVSM
 LTILYGYRWPLPSKLCVWYILDVLFSTASIMHLCAISLDTRYVAIQNPIHHSRFSRSTKAFLKIIAVW
 TISVGISMPIPVFGLQDDSKVFKEGSCLLADDNFVLIGSFVSFFIPLTIMVITYFLTIKVLRRQALMLL
 HGHTTEPPGLSLDFLKCCCKRNTAEENSANPNQDQONARRRKKKERRPRGTMQAINNERKAS
 KVLGIVFFLVVMWCPFFITNIMAVICKESCNEVDIGALLNVFVWIGYLSSAVNPLVYTLFNKIYR
 RAFSNYLRCNYKVEKKPPVRQIPRVAATALSGRELNVNIYRHTNEPVIEKASDNEPGIEMQVE
 NLELPVNPSSVVSERISSV

FIGURE 6C



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FIGURE 6A

ATGGATATTCTTTGTGAAGAAAATACTTCTTTGAGCTCAACTACGAACTCCCTAATGCAATTA
AATGATGACAACAGGCTCTACAGTAATGACTTTAACTCCGGAGAAGCTAACACTTCTGATGCA
TTTAACTGGACAGTCGACTCTGAAAATCGAACCAACCTTTCTGTGAAGGGTGCCTCTCACCG
TCGTGTCTCTCCTTACTTCATCTCCAGGAAAAAACTGGTCTGCTTTACTGACAGCCGTAGTGA
TTATTCTAACTATTGCTGGAAACATACTCGTCATCATGGCAGTGTCCCTAGAGAAAAAGCTGC
AGAATGCCACCAACTATTTCTGATGTCACTTGCCATAGCTGATATGCTGCTGGGTTTCTTGT
CATGCCCCGTGTCCATGTAAACCATCCTGTATGGGTACCGGTGGCCTCTGCCGAGCAAGCTTTGT
GCAGTCTGGATTTACCTGGACGTGCTCTTCTCCACGGCCTCCATCATGCACCTCTGCGCCATCT
CGCTGGACCGCTACGTGCGCCATCCAGAATCCCATCCACCACAGCCGCTTCAACTCCAGAACTA
AGGCATTTCTGAAAATCATTGCTGTTTGGACCATATCAGTAGGTATATCCATGCCAATACCAG
TCTTTGGGCTACAGGACGATTCTGAAGGTCTTTAAGGAGGGGAGTTGCTTACTCGCCGATGATA
ACTTTGTCCTGATCGGCTCTTTTGTGTCATTTTTCATTCCCTTAACCATCATGGTGATCACCTAC
TTTCTAACTATCAAGGTTCTGCGCCGACAAGCTTTGATGTTACTGCACGGCCACACCGAG
GAACCGCCTGGACTAAGTCTGGATTTCTGAAGTGCTGCAAGAGGAATACGGCCGAGGA
AGAGAACTCTGCAAACCCTAACCAAGACCAGAACGCACGCCGAAGAAAGAAGAAGGAG
AGACGTCCTAGGGGCACCATGCAGGCTATCAACAATGAAAGAAAAGCTTCGAAGGTACT
GGGCATCGTCTTCTTCCTGTTTGTGGTGATGTGGTGCCCTTTCTTCATCACAACATCATGGCC
GTCATCTGCAAAGAGTCCTGCAATGAGGATGTCAATTGGGGCCCTGCTCAATGTGTTTGTGTTGG
ATCGGTTATCTCTCTTCAGCAGTCAACCCACTAGTCTATACTCTGTTCAACAAAATTTACCGA
AGGGCATTCTCCAACCTATTTGCGTTGCAATTATAAGGTAGAGAAAAAGCCTCCTGTCAG
GCAGATTCCAAGAGTTGCCGCCACTGCTTTGTCTGGGAGGGAGCTTAATGTTAACATTT
ATCGGCATACCAATGAACCGGTGATCGAGAAAGCCAGTGACAATGAGCCCGGTATAGAG
ATGCAAGTTGAGAATTTAGAGTTACCAGTAAATCCCTCCAGTGTGGTTAGCGAAAGGAT
TAGCAGTGTGTGA

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FIGURE 7A

ATGGATATTCTTTGTGAAGAAAATACTTCTTTGAGCTCAACTACGAACTCCCTAATGCAATTA
AATGATGACAACAGGCTCTACAGTAATGACTTTAACTCCGGAGAAGCTAACACTTCTGATGCA
TTTAACTGGACAGTCGACTCTGAAAATCGAACCAACCTTTCCTGTGAAGGGTGCCTCTCACCG
TCGTGTCTCTCCTTACTTCATCTCCAGGAAAAAACTGGTCTGCTTTACTGACAGCCGTAGTGA
TTATTCTAACTATTGCTGGAAACATACTCGTCATCATGGCAGTGTCCCTAGAGAAAAAGCTGC
AGAATGCCACCAACTATTTCTGATGTCACTTGCCATAGCTGATATGCTGCTGGGTTTCCTTGT
CATGCCCGTGTCCATGTTAACCATCCTGTATGGGTACCGGTGGCCTCTGCCGAGCAAGCTTTGT
GCAGTCTGGATTTACCTGGACGTGCTCTTCTCCACGGCCTCCATCATGCACCTCTGCGCCATCT
CGCTGGACCGCTACGTCGCCATCCAGAATCCCATCCACCACAGCCGCTTCAACTCCAGAACTA
AGGCATTTCTGAAAATCATTGCTGTTTGGACCATATCAGTAGGTATATCCATGCCAATACCAG
TCTTTGGGCTACAGGACGATTCTGAAGGTCTTTAAGGAGGGGAGTTGCTTACTCGCCGATGATA
ACTTTGTCCTGATCGGCTCTTTTGTGTCATTTTTTCATTCCCCTGACGATTATGGTGATTACGT
ATTGCCTGACCATCTACGTTCTGCGCCGACAAGCTTTGATGTTACTGCACGGCCACACC
GAGGAACCGCCTGGACTAAGTCTGGATTTCTGAAGTGCTGCAAGAGGAATACGGCCGA
GGAAGAGAACTCTGCAAACCCTAACCAAGACCAGAACGCACGCCGAAGAAAGAAGAAG
GAGAGACGTCTAGGGGCACCATGCAGGCTATCAACAATGAAAGAAAAGCTAAGAAAGT
CCTTGGGATTGTTTTCTTTGTGTTTCTGATCATGTGGTGCCCTTTCTTCATCACAAACATCA
TGGCCGTCTCTGCAAAGAGTCCTGCAATGAGGATGTCATTGGGGCCCTGCTCAATGTGTTTG
TTGGATCGGTTATCTCTCTTCAGCAGTCAACCCACTAGTCTATACTCTGTTCAACAAAATTI
ACCGAAGGGCATTCTCCAATAATTGCGTTGCAATTATAAGGTAGAGAAAAAGCCTCCT
GTCAGGCAGATTCCAAGAGTTGCCGCCACTGCTTTGTCTGGGAGGGAGCTTAATGTTAA
CATTTATCGGCATACCAATGAACCGGTGATCGAGAAAGCCAGTGACAATGAGCCCGGTA
TAGAGATGCAAGTTGAGAATTTAGAGTTACCAGTAAATCCCTCCAGTGTGGTTAGCGAA
AGGATTAGCAGTGTGTGA

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FIGURE 7B

MDILCEENTSLSSTTNSLMQLNDDNRLYSNDFNSGEANTSDAFNWTVDSERNTNLSCEGCLSPSCL
 SLLHLQEKNEWSALLTAVVILTIAGNILVIMAVSLEKKLQATNYFLMSLAADMLLGFLVMPVSM
 LTILYGYRWPLPSKLCAVWTYLDVLFSTASIMHLCAISLDRYVAIQNPIHHSRFSRSTKAFLKIIAVW
 TISVGISMPIPVFGLQDDSKVFKEGSCLLADDNFVLIGSFVSFFIPLTIMVTITYCLTIYVLRROALML
LHGHTEEPGLSLDFLKCCCKRNTAEENSANPNODONARRRKKKERRRPRGTMOAINNERKA
KKVLGIVFFVFLIMWCPFFITNIMAVICKESCNEVDIGALLNVFVWIGYLSSAVNPLVYTLENKIY
RRAFSNYLRCNYKVEKKPPVROIPRVAATALSGRELNVNIYRHTNEPVIEKASDNEPGIEMOV
ENLELPVNPSSVVSERISSV

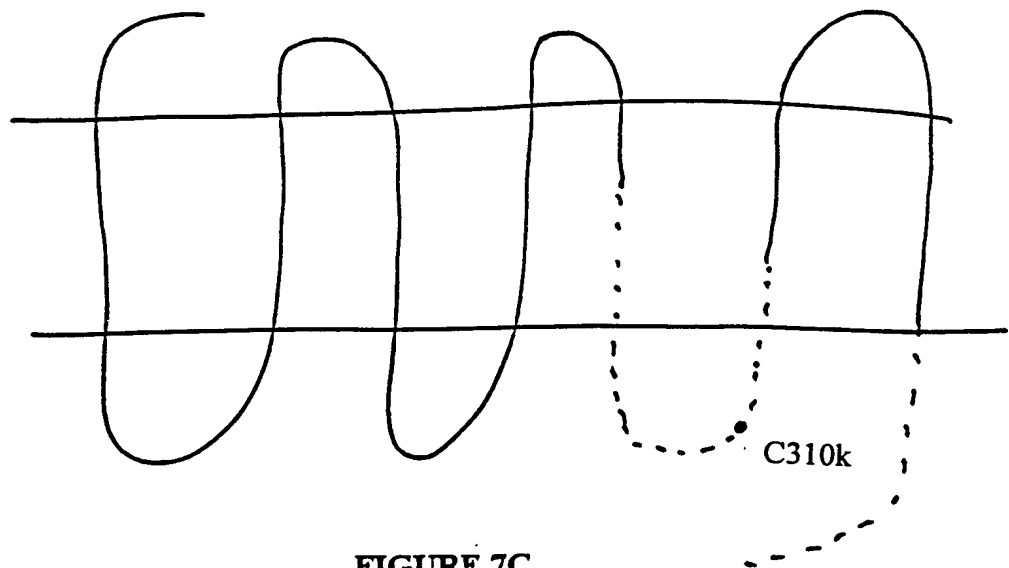


FIGURE 7C

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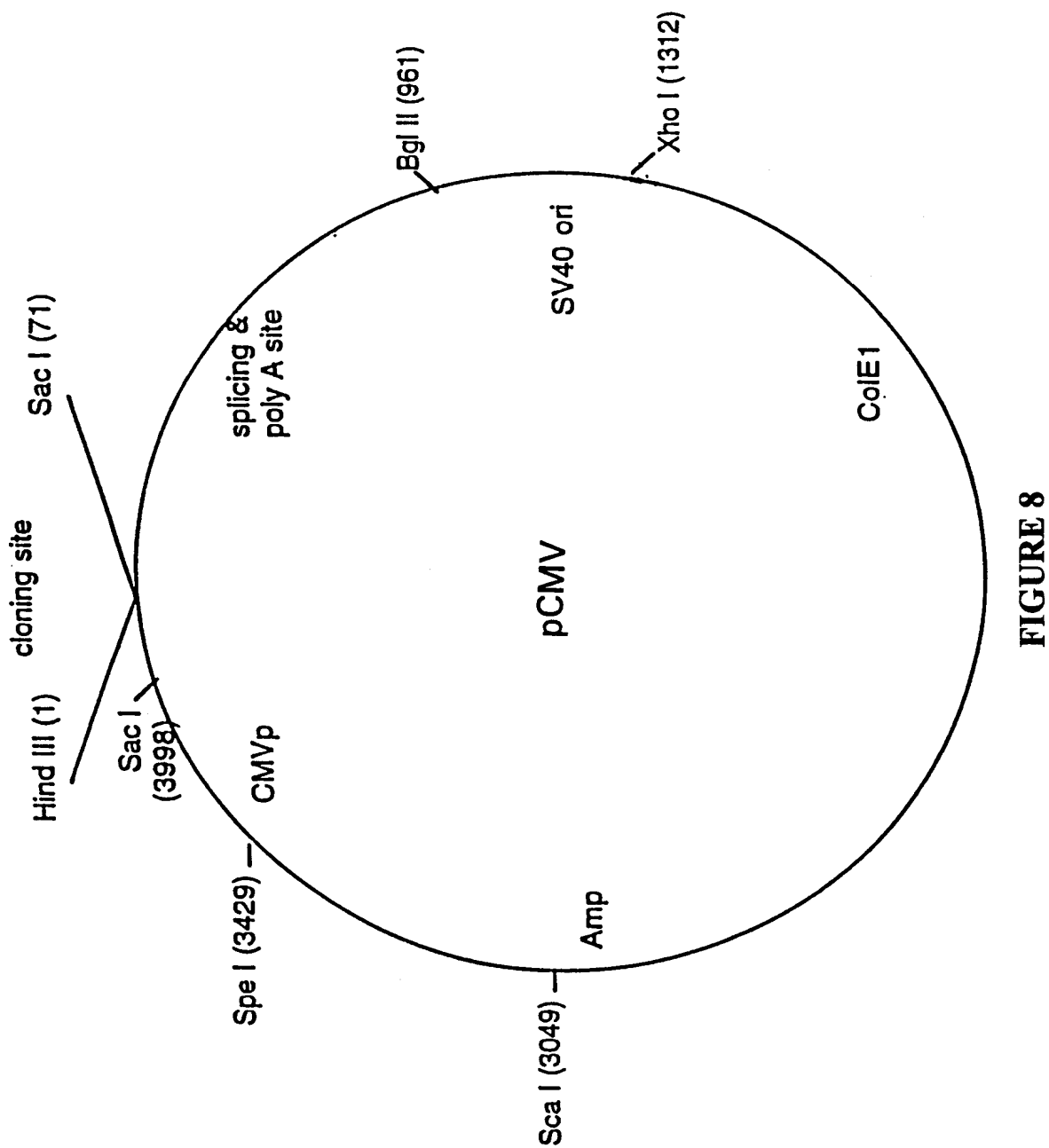


FIGURE 8

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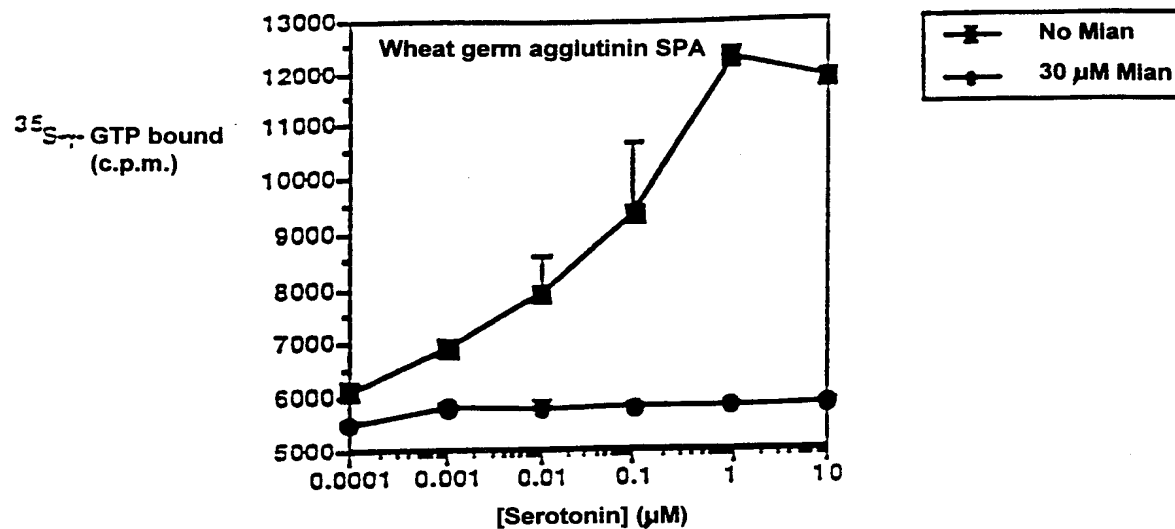


FIGURE 9

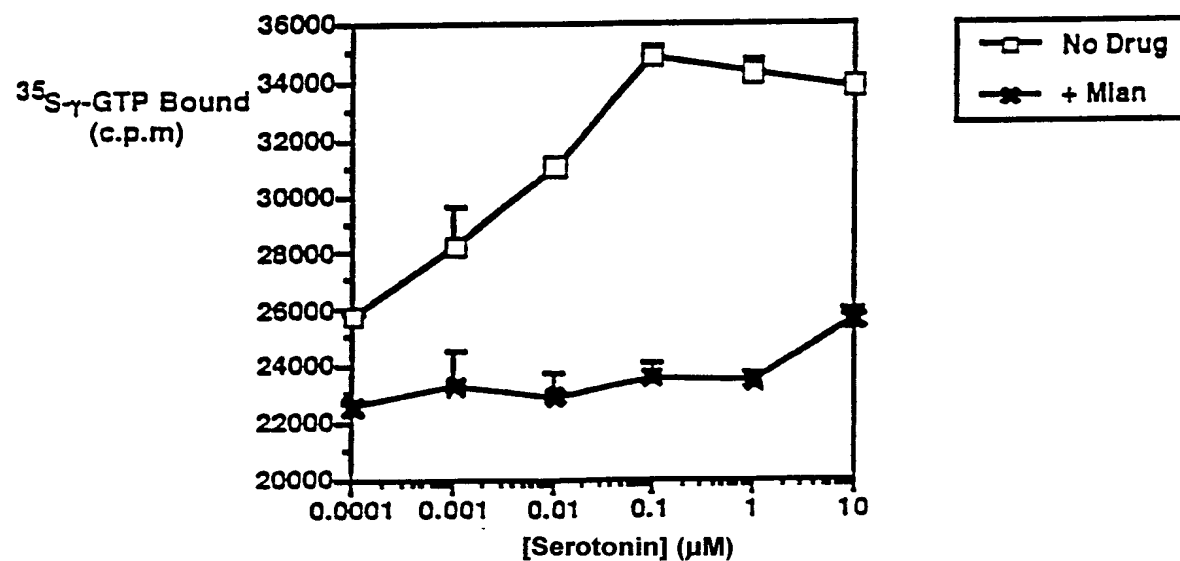


FIGURE 10

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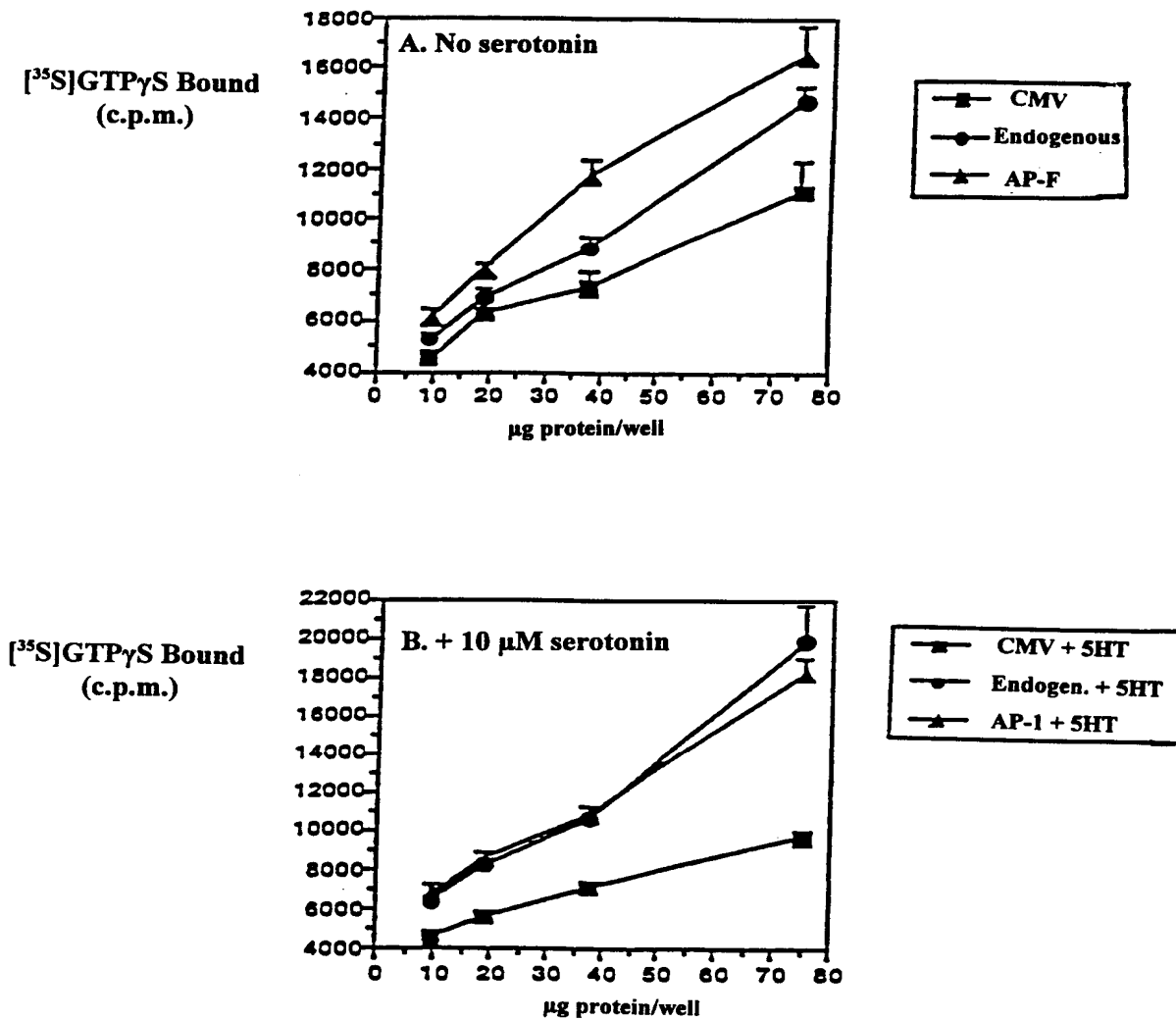


FIGURE 11

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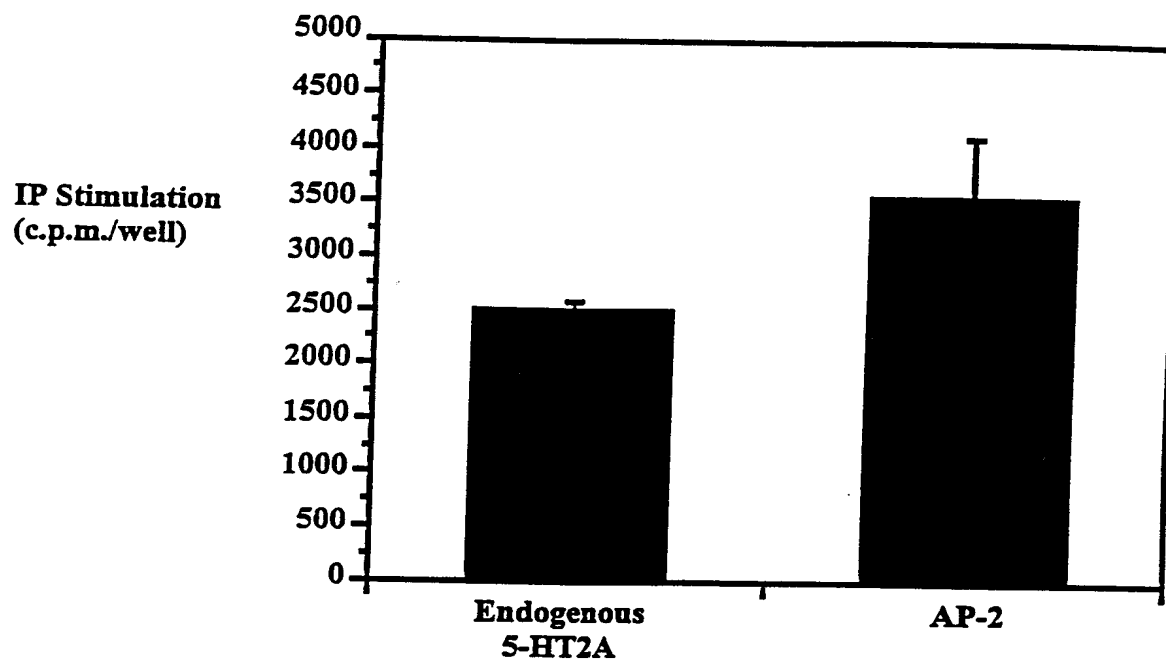


FIGURE 12

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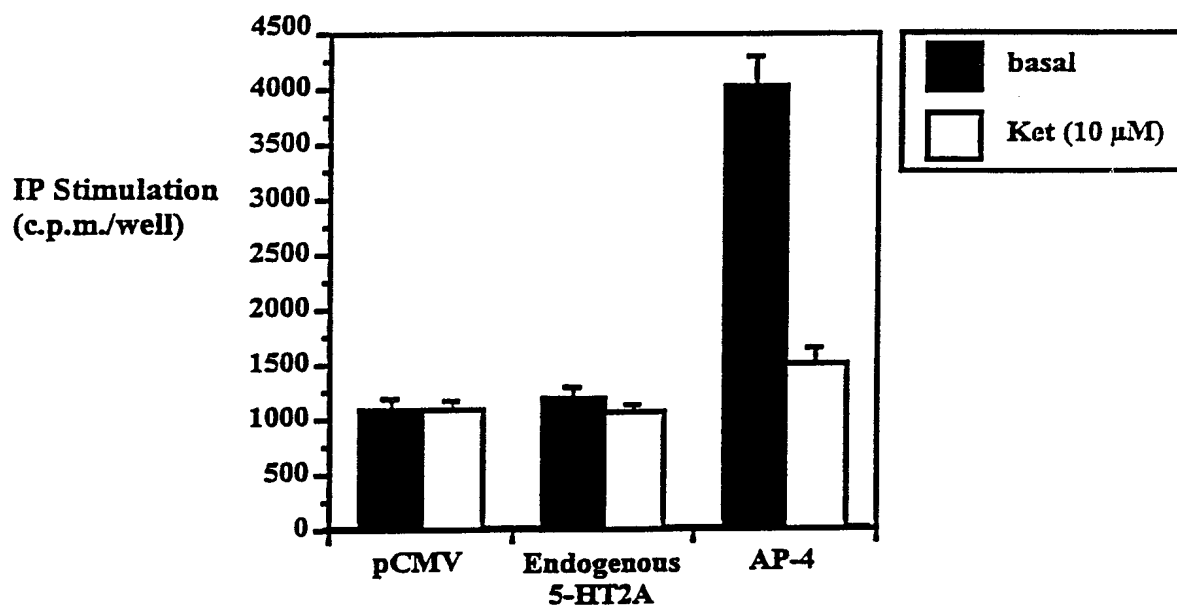


FIGURE 13

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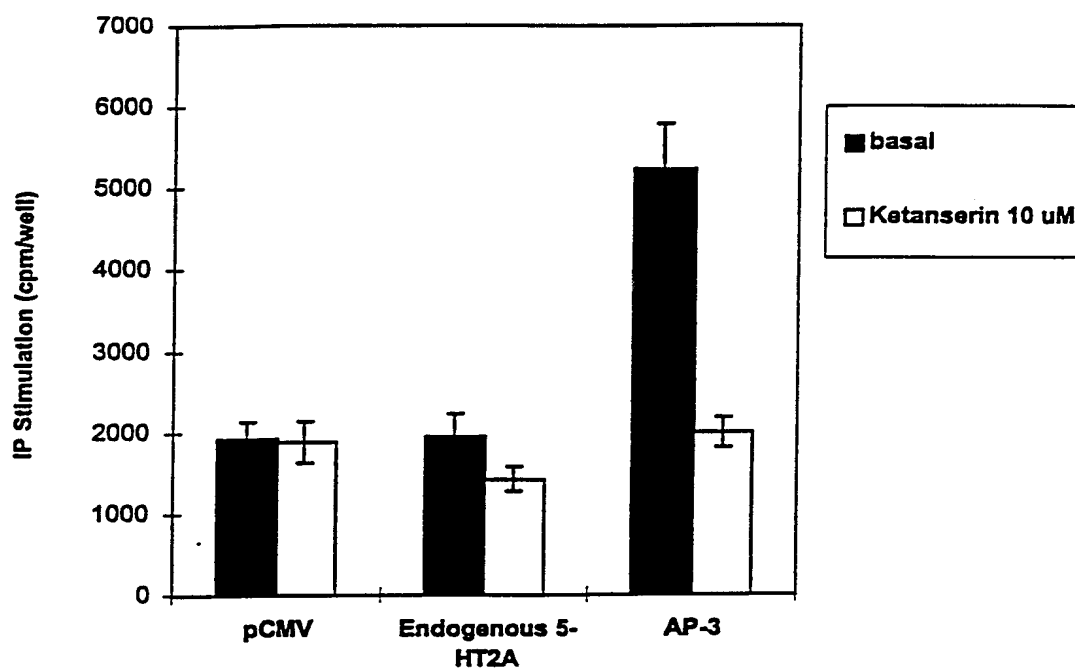


FIGURE 14

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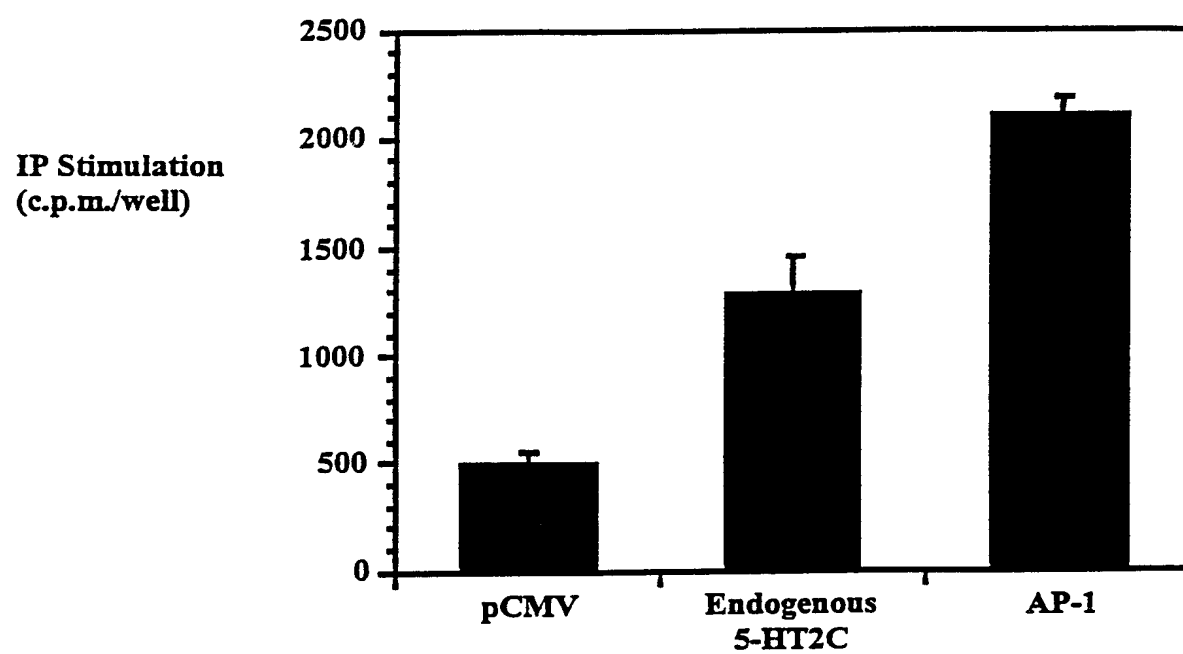


FIGURE 15

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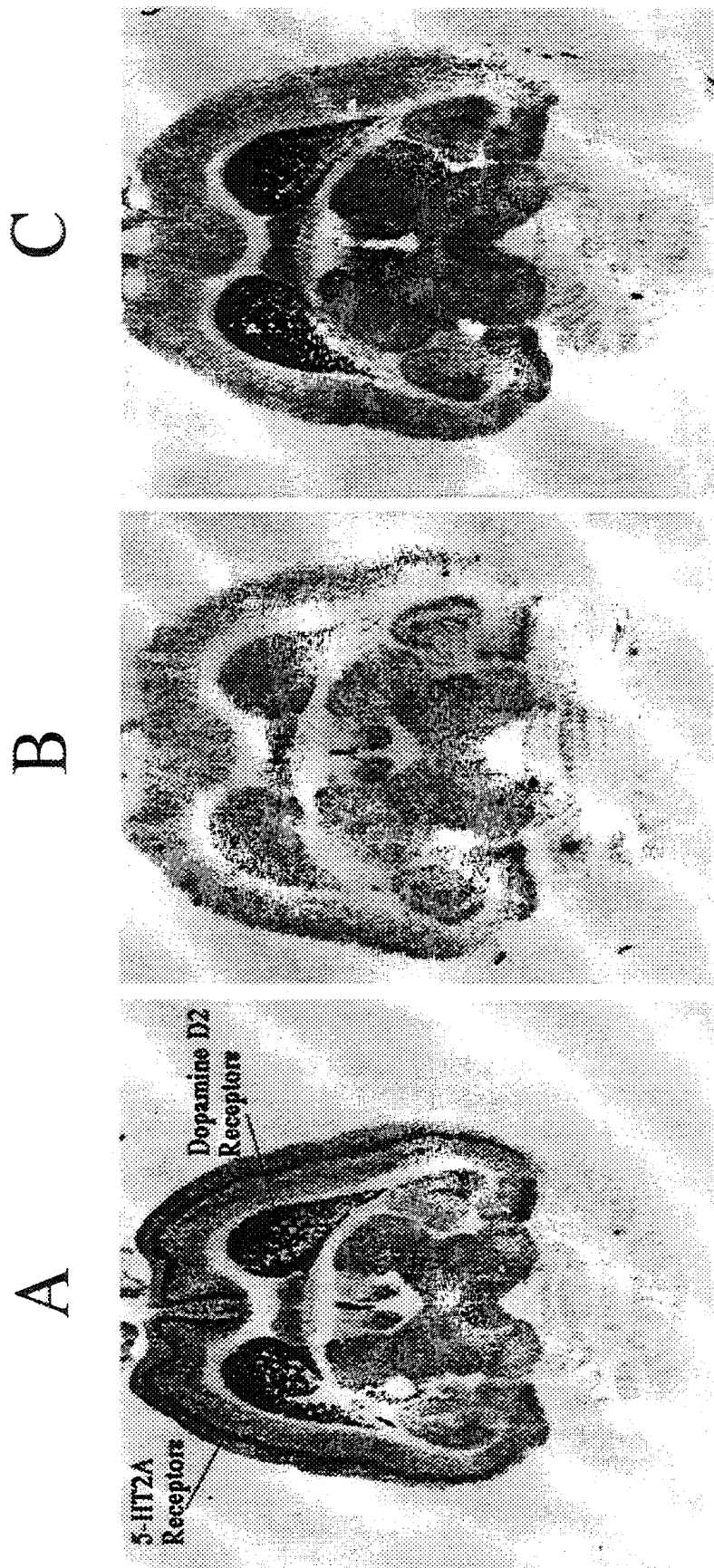


Figure 16

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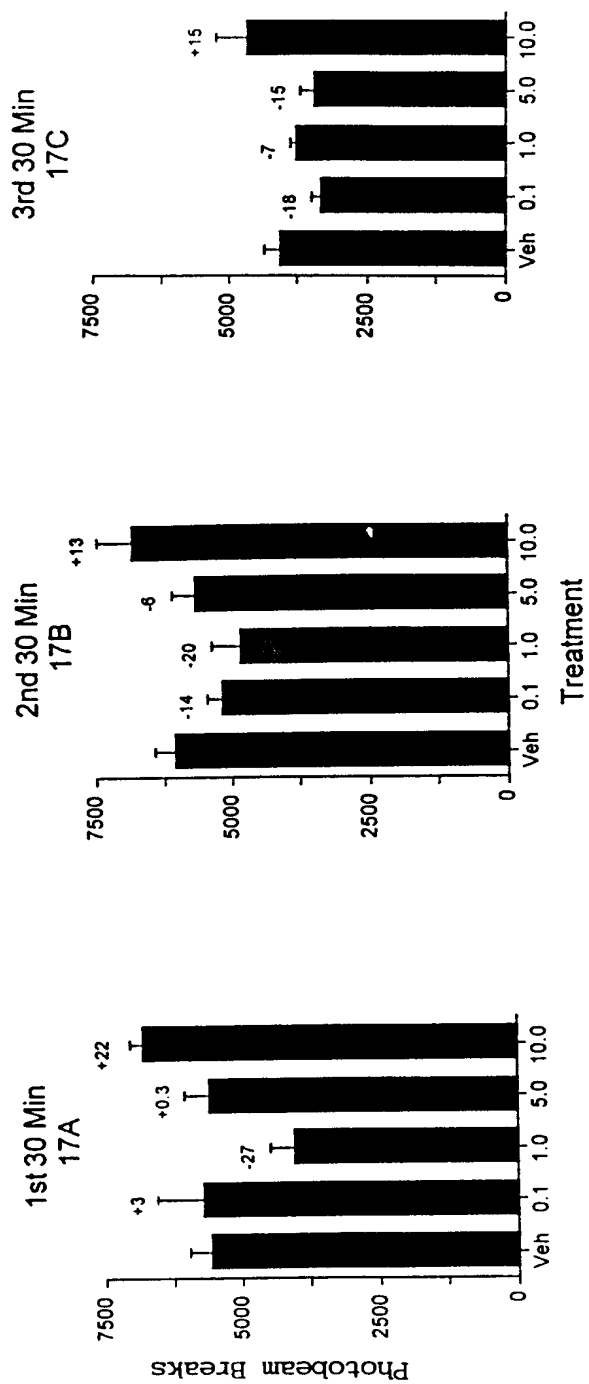


Figure 17

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Arena Pharmaceuticals, Inc. and Tripos, Inc.
- (ii) TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human Serotonin Receptors and Small Molecule Modulators Thereof
- (iii) NUMBER OF SEQUENCES: 33
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris LLP
 - (B) STREET: One Liberty Place - 46th Floor
 - (C) CITY: Philadelphia
 - (D) STATE: PA
 - (E) COUNTRY: USA
 - (F) ZIP: 19103
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: WINDOWS NT, Version #4.0
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US99/08168
 - (B) FILING DATE: April 14, 1999
 - (C) CLASSIFICATION: 435
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Mark J. Rosen
 - (B) REGISTRATION NUMBER: 39,822
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (215) 568-3100
 - (B) TELEFAX: (215) 568-3439

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GACCTCGAGG TTGCTTAAGA CTGAAGC

27

(3) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATTCTAGAC ATATGTAGCT TGTACCG

27

(4) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTAGGGGCAC CATGCAGGCT ATCAACAATG AAAGAAAAGC TAAGAAAGTC

50

(5) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAAGGACTTT CTTAGCTTTT CTTTCATTGT TGATAGCCTG CATGGTGCCC

50

(6) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACCTCGAGT CCTTCTACAC CTCATC

26

(7) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGCTCTAGAT TCCAGATAGG TGAAACTTG

30

(8) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAAAGAAAGT ACTGGGCATC GTCTTCTTCC T

31

(9) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGCTCGAGT ACTGCGCCGA CAAGCTTTGA T

31

(10) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGATGCCCGAG CACTTTCGAA GCTTTTCTTT CATTGTTG

38

(11) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AAAAGCTTCG AAAGTGCTGG GCATCGTCTT CTCCT

36

(12) INFORMATION FOR SEQ ID NO:11

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGCTCTAGAT TCCAGATAGG TGAAAACTTG

30

(13) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGTGTCTCTC CTTACTTCA

19

(14) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TCGGCGCAGT ACTTTGATAG TTAGAAAGTA GGTGAT

36

(15) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTCTAACTAT CAAAGTACTG CGCCGACAAG CTTTGATG

38

(16) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTCAGCAGTC AACCCACTAG TCTATACTCT GTTCAACAAA ATT

43

(17) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATTTCTAGAC ATATGTAGCT TGTACCGT

28

(18) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATCACCTACT TTCTAACTA

19

(19) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCATAATCGT CAGGGGAATG AAAAATGACA CAA

33

(20) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATTTTTCATT CCCCTGACGA TTATGGTGAT TAC

33

(21) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
TGATGAAGAA AGGGCACCAC ATGATCAGAA ACA 33
- (2) INFORMATION FOR SEQ ID NO:21:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
GATCATGTGG TGCCCTTTCT TCATCACAAA CAT 33
- (23) INFORMATION FOR SEQ ID NO:22:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
GAGACATATT ATCTGCCACG GAGG 24
- (24) INFORMATION FOR SEQ ID NO:23:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
TTGGCATAGA AACCGGACCC AAGG 24
- (25) INFORMATION FOR SEQ ID NO:24:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1416 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATGGATATTC TTTGTGAAGA AAATACTTCT TTGAGCTCAA CTACGAACTC CCTAATGCAA	60
TTAAATGATG ACAACAGGCT CTACAGTAAT GACTTTAACT CCGGAGAAGC TAACACTTCT	120
GATGCATTTA ACTGGACAGT CGACTCTGAA AATCGAACCA ACCTTTCCTG TGAAGGGTGC	180
CTCTCACCGT CGTGTCTCTC CTTACTTCAT CTCCAGGAAA AAAAC TGGTC TGCTTTACTG	240
ACAGCCGTAG TGATTATTCT AACTATTGCT GGAAACATAC TCGTCATCAT GGCAGTGTCC	300
CTAGAGAAAA AGCTGCAGAA TGCCACCAAC TATTTCTCTGA TGTCACCTGC CATAGCTGAT	360
ATGCTGCTGG GTTTCCTTGT CATGCCCGTG TCCATGTTAA CCATCCTGTA TGGGTACCGG	420
TGGCCTCTGC CGAGCAAGCT TTGTGCAGTC TGGATTTACC TGGACGTGCT CTTCTCCACG	480
GCCTCCATCA TGCACCTCTG CGCCATCTCG CTGGACCGCT ACGTCGCCAT CCAGAATCCC	540
ATCCACCACA GCCGCTTCAA CTCCAGAACT AAGGCATTTT TGAAAATCAT TGCTGTTTGG	600
ACCATATCAG TAGGTATATC CATGCCAATA CCAGTCTTTG GGCTACAGGA CGATTCTGAAG	660
GTCTTTAAGG AGGGGAGTTG CTTACTCGCC GATGATAACT TTGTCCTGAT CGGCTCTTTT	720
GTGTCATTTT TCATTCCCTT AACCATCATG GTGATCACCT ACTTTCTAAC TATCAAGTCA	780
CTCCAGAAAG AAGCTACTTT GTGTGTAAGT GATCTTGGCA CACGGGCCAA ATTAGCTTCT	840
TTCAGCTTCC TCCCTCAGAG TTCTTTGTCT TCAGAAAAGC TCTTCCAGCG GTCGATCCAT	900
AGGGAGCCAG GGTCTTACAC AGGCAGGAGG ACTATGCAGT CCATCAGCAA TGAGCAAAAG	960
GCATGCAAGG TGCTGGGCAT CGTCTTCTTC CTGTTTGTGG TGATGTGGTG CCCTTTCTTC	1020
ATCACAACA TCATGGCCGT CATCTGCAAA GAGTCCTGCA ATGAGGATGT CATTGGGGCC	1080

CTGCTCAATG TGTTTGTTTG GATCGGTTAT CTCTCTTCAG 1140
 CAGTCAACCC ACTAGTCTAC

ACACTGTTCA ACAAGACCTA TAGGTCAGCC TTTTCACGGT 1200
 ATATTCAGTG TCAGTACAAG

GAAAAACAAAA AACCATTTGCA GTTAATTTTA GTGAACACAA 1260
 TACCGGCTTT GGCCTACAAG

TCTAGCCAAC TTCAAATGGG ACAAAAAAAG AATTCAAAGC 1320
 AAGATGCCAA GACAACAGAT

AATGACTGCT CAATGGTTGC TCTAGGAAAG CAGTATTCTG 1380
 AAGAGGCTTC TAAAGACAAT

AGCGACGGAG TGAATGAAAA GGTGAGCTGT GTGTGA 1416

(26) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 470 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met	Asp	Ile	Leu	Cys	Glu	Glu	Asn	Thr	Ser	Leu	Ser	Ser	Thr	Thr	Asn	1	5	10	15
Ser	Leu	Met	Gln	Leu	Asn	Asp	Asp	Asn	Arg	Leu	Tyr	Ser	Asn	Asp	Phe	20	25	30	
Asn	Ser	Gly	Glu	Ala	Asn	Thr	Ser	Asp	Ala	Phe	Asn	Trp	Thr	Val	Asp	35	40	45	
Ser	Glu	Asn	Arg	Thr	Asn	Leu	Ser	Cys	Glu	Gly	Cys	Leu	Ser	Pro	Ser	50	55	60	
Cys	Ser	Leu	Leu	His	Leu	Gln	Glu	Lys	Asn	Trp	Ser	Ala	Leu	Leu	Thr	65	70	75	80
Ala	Val	Val	Ile	Ile	Leu	Thr	Ile	Ala	Gly	Asn	Ile	Leu	Val	Ile	Met	85	90	95	
Ala	Val	Ser	Leu	Glu	Lys	Lys	Leu	Gln	Asn	Ala	Thr	Asn	Tyr	Phe	Leu	100	105	110	
Met	Ser	Leu	Ala	Ile	Ala	Asp	Met	Leu	Leu	Gly	Phe	Leu	Val	Met	Pro	115	120	125	
Val	Ser	Met	Leu	Thr	Ile	Leu	Tyr	Gly	Tyr	Arg	Trp	Pro	Leu	Pro	Ser	130	135	140	
Lys	Leu	Cys	Ala	Val	Trp	Ile	Tyr	Leu	Asp	Val	Leu	Phe	Ser	Thr	Ala	145	150	155	160

Ser Ile Met His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala Ile
 165 170 175
 Gln Asn Pro Ile His His Ser Arg Phe Asn Ser Arg Thr Lys Ala Phe
 180 185 190
 Leu Lys Ile Ile Ala Val Trp Thr Ile Ser Val Gly Ile Ser Met Pro
 195 200 205
 Ile Pro Val Phe Gly Leu Gln Asp Asp Ser Lys Val Phe Lys Glu Gly
 210 215 220
 Ser Cys Leu Leu Ala Asp Asp Asn Phe Val Leu Ile Gly Ser Phe Val
 225 230 235 240
 Ser Phe Phe Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Phe Leu Thr
 245 250 255
 Ile Lys Ser Leu Gln Lys Glu Ala Thr Leu Cys Val Ser Asp Leu Gly
 260 265 270
 Thr Arg Ala Lys Leu Ala Ser Phe Ser Phe Leu Pro Gln Ser Ser Leu
 275 280 285
 Ser Ser Glu Lys Leu Phe Gln Arg Ser Ile His Arg Glu Pro Gly Ser
 290 295 300
 Tyr Thr Gly Arg Arg Thr Met Gln Ser Ile Ser Asn Glu Gln Lys Ala
 305 310 315 320
 Cys Lys Val Leu Gly Ile Val Phe Phe Leu Phe Val Val Met Trp Cys
 325 330 335
 Pro Phe Phe Ile Thr Asn Ile Met Ala Val Ile Cys Lys Glu Ser Cys
 340 345 350
 Asn Glu Asp Val Ile Gly Ala Leu Leu Asn Val Phe Val Trp Ile Gly
 355 360 365
 Tyr Leu Ser Ser Ala Val Asn Pro Leu Val Tyr Thr Leu Phe Asn Lys
 370 375 380
 Thr Tyr Arg Ser Ala Phe Ser Arg Tyr Ile Gln Cys Gln Tyr Lys Glu
 385 390 395 400
 Asn Lys Lys Pro Leu Gln Leu Ile Leu Val Asn Thr Ile Pro Ala Leu
 405 410 415
 Ala Tyr Lys Ser Ser Gln Leu Gln Met Gly Gln Lys Lys Asn Ser Lys
 420 425 430
 Gln Asp Ala Lys Thr Thr Asp Asn Asp Cys Ser Met Val Ala Leu Gly
 435 440 445
 Lys Gln Tyr Ser Glu Glu Ala Ser Lys Asp Asn Ser Asp Gly Val Asn
 450 455 460
 Glu Lys Val Ser Cys Val
 465 470

(27) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATGGTGAACC TGAGGAATGC GGTGCATTCA TTCCTTGTGC ACCTAATTGG CCTATTGGTT	60
TGGCAATGTG ATATTTCTGT GAGCCCAGTA GCAGCTATAG TAACTGACAT TTTCAATACC	120
TCCGATGGTG GACGCTTCAA ATTCCCAGAC GGGGTACAAA ACTGGCCAGC ACTTTCAATC	180
GTCATCATAA TAATCATGAC AATAGGTGGC AACATCCTTG TGATCATGGC AGTAAGCATG	240
GAAAAGAAAC TGCACAATGC CACCAATTAC TTCTTAATGT CCCTAGCCAT TGCTGATATG	300
CTAGTGGGAC TACTTGT CAT GCCCCTGTCT CTCCTGGCAA TCCTTTATGA TTATGTCTGG	360
CCACTACCTA GATATTTGTG CCCCGTCTGG ATTTCTTTAG ATGTTTTATT TTCAACAGCG	420
TCCATCATGC ACCTCTGCGC TATATCGCTG GATCGGTATG TAGCAATACG TAATCCTATT	480
GAGCATAGCC GTTTCAATTC GCGGACTAAG GCCATCATGA AGATTGCTAT TGTTTGGGCA	540
ATTTCTATAG GTGTATCAGT TCCTATCCCT GTGATTGGAC TGAGGGACGA AGAAAAGGTG	600
TTCGTGAACA ACACGACGTG CGTGCTCAAC GACCCAAATT TCGTTCTTAT TGGGTCCTTC	660
GTAGCTTTCT TCATACCGCT GACGATTATG GTGATTACGT ATTGCCTGAC CATCTACGTT	720
CTGCGCCGAC AAGCTTTGAT GTTACTGCAC GGCCACACCG AGGAACCGCC TGGACTAAGT	780
CTGGATTTC TGAAGTGCTG CAAGAGGAAT ACGGCCGAGG AAGAGAACTC TGCAAACCCT	840
AACCAAGACC AGAACGCACG CCGAAGAAAG AAGAAGGAGA GACGTCCTAG GGGCACCATG	900
CAGGCTATCA ACAATGAAAG AAAAGCTTCG AAAGTCCTTG GGATTGTTTT CTTTGTGTTT	960
CTGATCATGT GGTGCCCAT TTTCAATTACC AATATTCTGT CTGTTCTTTG TGAGAAGTCC	1020
TGTAACCAAA AGCTCATGGA AAAGCTTCTG AATGTGTTTG TTTGGATTGG CTATGTTTGT	1080
TCAGGAATCA ATCCTCTGGT GTATACTCTG TTCAACAAAA TTTACCGAAG GGCATTCTCC	1140
AACTATTTGC GTTGCAATTA TAAGGTAGAG AAAAAGCCTC CTGTCAGGCA GATTCCAAGA	1200
GTTGCCGCCA CTGCTTTGTC TGGGAGGGAG CTTAATGTTA ACATTTATCG GCATACCAAT	1260
GAACCGGTGA TCGAGAAAGC CAGTGACAAT GAGCCCGGTA TAGAGATGCA AGTTGAGAAT	1320
TTAGAGTTAC CAGTAAATCC CTCCAGTGTG GTTAGCGAAA GGATTAGCAG TGTGTGA	1377

(28) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

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Met Val Asn Leu Arg Asn Ala Val His Ser Phe Leu Val His Leu Ile
1           5           10           15

Gly Leu Leu Val Trp Gln Cys Asp Ile Ser Val Ser Pro Val Ala Ala
20           25           30

Ile Val Thr Asp Ile Phe Asn Thr Ser Asp Gly Gly Arg Phe Lys Phe
35           40           45

Pro Asp Gly Val Gln Asn Trp Pro Ala Leu Ser Ile Val Ile Ile Ile
50           55           60

Ile Met Thr Ile Gly Gly Asn Ile Leu Val Ile Met Ala Val Ser Met
65           70           75           80

Glu Lys Lys Leu His Asn Ala Thr Asn Tyr Phe Leu Met Ser Leu Ala
85           90           95

Ile Ala Asp Met Leu Val Gly Leu Leu Val Met Pro Leu Ser Leu Leu
100          105          110

Ala Ile Leu Tyr Asp Tyr Val Trp Pro Leu Pro Arg Tyr Leu Cys Pro
115          120          125

Val Trp Ile Ser Leu Asp Val Leu Phe Ser Thr Ala Ser Ile Met His
130          135          140

Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala Ile Arg Asn Pro Ile
145          150          155          160

Glu His Ser Arg Phe Asn Ser Arg Thr Lys Ala Ile Met Lys Ile Ala
165          170          175

Ile Val Trp Ala Ile Ser Ile Gly Val Ser Val Pro Ile Pro Val Ile
180          185          190

Gly Leu Arg Asp Glu Glu Lys Val Phe Val Asn Asn Thr Thr Cys Val
195          200          205

Leu Asn Asp Pro Asn Phe Val Leu Ile Gly Ser Phe Val Ala Phe Phe
210          215          220

Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Cys Leu Thr Ile Tyr Val
225          230          235          240

Leu Arg Arg Gln Ala Leu Met Leu Leu His Gly His Thr Glu Glu Pro
245          250          255

Pro Gly Leu Ser Leu Asp Phe Leu Lys Cys Cys Lys Arg Asn Thr Ala
260          265          270

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Glu Glu Glu Asn Ser Ala Asn Pro Asn Gln Asp Gln Asn Ala Arg Arg
 275 280 285
 Arg Lys Lys Lys Glu Arg Arg Pro Arg Gly Thr Met Gln Ala Ile Asn
 290 295 300
 Asn Glu Arg Lys Ala Ser Lys Val Leu Gly Ile Val Phe Phe Val Phe
 305 310 315 320
 Leu Ile Met Trp Cys Pro Phe Phe Ile Thr Asn Ile Leu Ser Val Leu
 325 330 335
 Cys Glu Lys Ser Cys Asn Gln Lys Leu Met Glu Lys Leu Leu Asn Val
 340 345 350
 Phe Val Trp Ile Gly Tyr Val Cys Ser Gly Ile Asn Pro Leu Val Tyr
 355 360 365
 Thr Leu Phe Asn Lys Ile Tyr Arg Arg Ala Phe Ser Asn Tyr Leu Arg
 370 375 380
 Cys Asn Tyr Lys Val Glu Lys Lys Pro Pro Val Arg Gln Ile Pro Arg
 385 390 395 400
 Val Ala Ala Thr Ala Leu Ser Gly Arg Glu Leu Asn Val Asn Ile Tyr
 405 410 415
 Arg His Thr Asn Glu Pro Val Ile Glu Lys Ala Ser Asp Asn Glu Pro
 420 425 430
 Gly Ile Glu Met Gln Val Glu Asn Leu Glu Leu Pro Val Asn Pro Ser
 435 440 445
 Ser Val Val Ser Glu Arg Ile Ser Ser Val
 450 455

(29) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATGGTGAACC TGAGGAATGC GGTGCATTCA TTCCTTGTGC ACCTAATTGG CCTATTGGTT	60
TGGCAATGTG ATATTTCTGT GAGCCCAGTA GCAGCTATAG TAACTGACAT TTTCAATACC	120
TCCGATGGTG GACGCTTCAA ATTCCCAGAC GGGGTACAAA ACTGGCCAGC ACTTTCAATC	180
GTCATCATAA TAATCATGAC AATAGGTGGC AACATCCTTG TGATCATGGC AGTAAGCATG	240
GAAAAGAAAC TGCACAATGC CACCAATTAC TTCTTAATGT CCCTAGCCAT TGCTGATATG	300
CTAGTGGGAC TACTTGTCAT GCCCCTGTCT CTCCTGGCAA TCCTTTATGA TTATGTCTGG	360

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CCACTACCTA GATATTTGTG CCCCGTCTGG ATTTCTTTAG ATGTTTTATT TTCAACAGCG      420
TCCATCATGC ACCTCTGCGC TATATCGCTG GATCGGTATG TAGCAATACG TAATCCTATT      480
GAGCATAGCC GTTTC AATTC GCGGACTAAG GCCATCATGA AGATTGCTAT TGT TTGGGCA      540
ATTTCTATAG GTGTATCAGT TCCTATCCCT GTGATTGGAC TGAGGGACGA AGAAAAGGTG      600
TTCGTGAACA ACACGACGTG CGTGCTCAAC GACCCAAATT TCGTTCTTAT TGGGTCCTTC      660
GTAGCTTTCT TCATACCGCT GACGATTATG GTGATTACGT ATTGCCTGAC CATCTACGTT      720
CTGCGCCGAC AAGCTTTGAT GTTACTGCAC GGCCACACCG AGGAACCGCC TGGACTAAGT      780
CTGGATTTC TGAAGTGCTG CAAGAGGAAT ACGGCCGAGG AAGAGAACTC TGCAAACCCCT      840
AACCAAGACC AGAACGCACG CCGAAGAAAG AAGAAGGAGA GACGTCCTAG GGGCACCATG      900
CAGGCTATCA ACAATGAAAG AAAAGCTAAG AAAGTCCTTG GGATTGTTTT CTTTGTGTTT      960
CTGATCATGT GGTGCCCATT TTTCATTACC AATATTCTGT CTGTTCTTTG TGAGAAGTCC     1020
TGTAACCAAA AGCTCATGGA AAAGCTTCTG AATGTGTTTG TTTGGATTGG CTATGTTTGT     1080
TCAGGAATCA ATCCTCTGGT GTATACTCTG TTCAACAAAA TTTACCGAAG GGCATTCTCC     1140
AACTATTTGC GTTGCAATTA TAAGGTAGAG AAAAAGCCTC CTGTCAGGCA GATTCCAAGA     1200
GTTGCCGCCA CTGCTTTGTC TGGGAGGGAG CTTAATGTTA ACATTTATCG GCATACCAAT     1260
GAACCGGTGA TCGAGAAAGC CAGTGACAAT GAGCCCGGTA TAGAGATGCA AGTTGAGAAT     1320
TTAGAGTTAC CAGTAAATCC CTCCAGTGTG GTTAGCGAAA GGATTAGCAG TGTGTGA       1377

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(30) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 458 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

Met Val Asn Leu Arg Asn Ala Val His Ser Phe Leu Val His Leu Ile
1           5           10           15
Gly Leu Leu Val Trp Gln Cys Asp Ile Ser Val Ser Pro Val Ala Ala
20           25           30
Ile Val Thr Asp Ile Phe Asn Thr Ser Asp Gly Gly Arg Phe Lys Phe
35           40           45
Pro Asp Gly Val Gln Asn Trp Pro Ala Leu Ser Ile Val Ile Ile Ile
50           55           60
Ile Met Thr Ile Gly Gly Asn Ile Leu Val Ile Met Ala Val Ser Met

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65	70	75	80
Glu Lys Lys Leu His Asn Ala Thr Asn Tyr Phe Leu Met Ser Leu Ala	85	90	95
Ile Ala Asp Met Leu Val Gly Leu Leu Val Met Pro Leu Ser Leu Leu	100	105	110
Ala Ile Leu Tyr Asp Tyr Val Trp Pro Leu Pro Arg Tyr Leu Cys Pro	115	120	125
Val Trp Ile Ser Leu Asp Val Leu Phe Ser Thr Ala Ser Ile Met His	130	135	140
Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala Ile Arg Asn Pro Ile	145	150	155
Glu His Ser Arg Phe Asn Ser Arg Thr Lys Ala Ile Met Lys Ile Ala	165	170	175
Ile Val Trp Ala Ile Ser Ile Gly Val Ser Val Pro Ile Pro Val Ile	180	185	190
Gly Leu Arg Asp Glu Glu Lys Val Phe Val Asn Asn Thr Thr Cys Val	195	200	205
Leu Asn Asp Pro Asn Phe Val Leu Ile Gly Ser Phe Val Ala Phe Phe	210	215	220
Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Cys Leu Thr Ile Tyr Val	225	230	235
Leu Arg Arg Gln Ala Leu Met Leu Leu His Gly His Thr Glu Glu Pro	245	250	255
Pro Gly Leu Ser Leu Asp Phe Leu Lys Cys Cys Lys Arg Asn Thr Ala	260	265	270
Glu Glu Glu Asn Ser Ala Asn Pro Asn Gln Asp Gln Asn Ala Arg Arg	275	280	285
Arg Lys Lys Lys Glu Arg Arg Pro Arg Gly Thr Met Gln Ala Ile Asn	290	295	300
Asn Glu Arg Lys Ala Lys Lys Val Leu Gly Ile Val Phe Phe Val Phe	305	310	315
Leu Ile Met Trp Cys Pro Phe Phe Ile Thr Asn Ile Leu Ser Val Leu	325	330	335
Cys Glu Lys Ser Cys Asn Gln Lys Leu Met Glu Lys Leu Leu Asn Val	340	345	350
Phe Val Trp Ile Gly Tyr Val Cys Ser Gly Ile Asn Pro Leu Val Tyr	355	360	365
Thr Leu Phe Asn Lys Ile Tyr Arg Arg Ala Phe Ser Asn Tyr Leu Arg	370	375	380
Cys Asn Tyr Lys Val Glu Lys Lys Pro Pro Val Arg Gln Ile Pro Arg	385	390	395
			400

Val Ala Ala Thr Ala Leu Ser Gly Arg Glu Leu Asn Val Asn Ile Tyr
 405 410 415

Arg His Thr Asn Glu Pro Val Ile Glu Lys Ala Ser Asp Asn Glu Pro
 420 425 430

Gly Ile Glu Met Gln Val Glu Asn Leu Glu Leu Pro Val Asn Pro Ser
 435 440 445

Ser Val Val Ser Glu Arg Ile Ser Ser Val
 450 455

(31) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1437 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATGGATATTC TTTGTGAAGA AAATACTTCT TTGAGCTCAA CTACGAACTC CCTAATGCAA	60
TTAAATGATG ACAACAGGCT CTACAGTAAT GACTTTAACT CCGGAGAAGC TAACACTTCT	120
GATGCATTTA ACTGGACAGT CGACTCTGAA AATCGAACCA ACCTTTCCTG TGAAGGGTGC	180
CTCTCACCGT CGTGTCTCTC CTTACTTCAT CTCCAGGAAA AAAACTGGTC TGCTTTACTG	240
ACAGCCGTAG TGATTATTCT AACTATTGCT GGAAACATAC TCGTCATCAT GGCAGTGTCC	300
CTAGAGAAAA AGCTGCAGAA TGCCACCAAC TATTTCTGA TGTCACTTGC CATAGCTGAT	360
ATGCTGCTGG GTTTCCTTGT CATGCCCGTG TCCATGTTAA CCATCCTGTA TGGGTACCGG	420
TGGCCTCTGC CGAGCAAGCT TTGTGCAGTC TGGATTTACC TGGACGTGCT CTTCTCCACG	480
GCCTCCATCA TGCACCTCTG CGCCATCTCG CTGGACCGCT ACGTCGCCAT CCAGAATCCC	540
ATCCACCACA GCCGCTTCAA CTCCAGAACT AAGGCATTTT TGAAAATCAT TGCTGTTTGG	600
ACCATATCAG TAGGTATATC CATGCCAATA CCAGTCTTTG GGCTACAGGA CGATTCTGAAG	660
GTCTTTAAGG AGGGGAGTTG CTTACTCGCC GATGATAACT TTGTCCTGAT CGGCTCTTTT	720
GTGTCATTTT TCATTCCCTT AACCATCATG GTGATCACCT ACTTTCTAAC TATCAAGGTT	780
CTGCGCCGAC AAGCTTTGAT GTTACTGCAC GGCCACACCG AGGAACCGCC TGGACTAAGT	840
CTGGATTTCC TGAAGTGCTG CAAGAGGAAT ACGGCCGAGG AAGAGAACTC TGCAAACCCT	900
AACCAAGACC AGAACGCACG CCGAAGAAAG AAGAAGGAGA GACGTCCTAG GGGCACCATG	960
CAGGCTATCA ACAATGAAAG AAAAGCTTCG AAGGTACTGG GCATCGTCTT CTTCTGTTTT	1020
GTGGTGATGT GGTGCCCTTT CTTTCATCACA AACATCATGG CCGTCATCTG CAAAGAGTCC	1080

TGCAATGAGG ATGTCATTGG GGCCCTGCTC AATGTGTTTG TTTGGATCGG TTATCTCTCT 1140
 TCAGCAGTCA ACCCACTAGT CTATACTCTG TTCAACAAAA TTTACCGAAG GGCATTCTCC 1200
 AACTATTTGC GTTGCAATTA TAAGGTAGAG AAAAAGCCTC CTGTCAGGCA GATTCCAAGA 1260
 GTTGCCGCCA CTGCTTTGTC TGGGAGGGAG CTTAATGTGA ACATTTATCG GCATACCAAT 1320
 GAACCGGTGA TCGAGAAAGC CAGTGACAAT GAGCCCGGTA TAGAGATGCA AGTTGAGAAT 1380
 TTAGAGTTAC CAGTAAATCC CTCCAGTGTG GTTAGCGAAA GGATTAGCAG TGTGTGA 1437

(32) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 478 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met	Asp	Ile	Leu	Cys	Glu	Glu	Asn	Thr	Ser	Leu	Ser	Ser	Thr	Thr	Asn	1	5	10	15
Ser	Leu	Met	Gln	Leu	Asn	Asp	Asp	Asn	Arg	Leu	Tyr	Ser	Asn	Asp	Phe	20	25	30	
Asn	Ser	Gly	Glu	Ala	Asn	Thr	Ser	Asp	Ala	Phe	Asn	Trp	Thr	Val	Asp	35	40	45	
Ser	Glu	Asn	Arg	Thr	Asn	Leu	Ser	Cys	Glu	Gly	Cys	Leu	Ser	Pro	Ser	50	55	60	
Cys	Leu	Ser	Leu	Leu	His	Leu	Gln	Glu	Lys	Asn	Trp	Ser	Ala	Leu	Leu	65	70	75	80
Thr	Ala	Val	Val	Ile	Ile	Leu	Thr	Ile	Ala	Gly	Asn	Ile	Leu	Val	Ile	85	90	95	
Met	Ala	Val	Ser	Leu	Glu	Lys	Lys	Leu	Gln	Asn	Ala	Thr	Asn	Tyr	Phe	100	105	110	
Leu	Met	Ser	Leu	Ala	Ile	Ala	Asp	Met	Leu	Leu	Gly	Phe	Leu	Val	Met	115	120	125	
Pro	Val	Ser	Met	Leu	Thr	Ile	Leu	Tyr	Gly	Tyr	Arg	Trp	Pro	Leu	Pro	130	135	140	
Ser	Lys	Leu	Cys	Ala	Val	Trp	Ile	Tyr	Leu	Asp	Val	Leu	Phe	Ser	Thr	145	150	155	160
Ala	Ser	Ile	Met	His	Leu	Cys	Ala	Ile	Ser	Leu	Asp	Arg	Tyr	Val	Ala	165	170	175	
Ile	Gln	Asn	Pro	Ile	His	His	Ser	Arg	Phe	Asn	Ser	Arg	Thr	Lys	Ala	180	185	190	

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Phe Leu Lys Ile Ile Ala Val Trp Thr Ile Ser Val Gly Ile Ser Met
    195                                200                                205

Pro Ile Pro Val Phe Gly Leu Gln Asp Asp Ser Lys Val Phe Lys Glu
    210                                215                                220

Gly Ser Cys Leu Leu Ala Asp Asp Asn Phe Val Leu Ile Gly Ser Phe
    225                                230                                235                                240

Val Ser Phe Phe Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Phe Leu
                245                                250                                255

Thr Ile Lys Val Leu Arg Arg Gln Ala Leu Met Leu Leu His Gly His
                260                                265                                270

Thr Glu Glu Pro Pro Gly Leu Ser Leu Asp Phe Leu Lys Cys Cys Lys
                275                                280                                285

Arg Asn Thr Ala Glu Glu Glu Asn Ser Ala Asn Pro Asn Gln Asp Gln
    290                                295                                300

Asn Ala Arg Arg Arg Lys Lys Lys Glu Arg Arg Pro Arg Gly Thr Met
    305                                310                                315                                320

Gln Ala Ile Asn Asn Glu Arg Lys Ala Ser Lys Val Leu Gly Ile Val
                325                                330                                335

Phe Phe Leu Phe Val Val Met Trp Cys Pro Phe Phe Ile Thr Asn Ile
                340                                345                                350

Met Ala Val Ile Cys Lys Glu Ser Cys Asn Glu Asp Val Ile Gly Ala
                355                                360                                365

Leu Leu Asn Val Phe Val Trp Ile Gly Tyr Leu Ser Ser Ala Val Asn
    370                                375                                380

Pro Leu Val Tyr Thr Leu Phe Asn Lys Ile Tyr Arg Arg Ala Phe Ser
    385                                390                                395                                400

Asn Tyr Leu Arg Cys Asn Tyr Lys Val Glu Lys Lys Pro Pro Val Arg
                405                                410                                415

Gln Ile Pro Arg Val Ala Ala Thr Ala Leu Ser Gly Arg Glu Leu Asn
                420                                425                                430

Val Asn Ile Tyr Arg His Thr Asn Glu Pro Val Ile Glu Lys Ala Ser
                435                                440                                445

Asp Asn Glu Pro Gly Ile Glu Met Gln Val Glu Asn Leu Glu Leu Pro
    450                                455                                460

Val Asn Pro Ser Ser Val Val Ser Glu Arg Ile Ser Ser Val
    465                                470                                475

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(33) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1437 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATGGATATTC TTTGTGAAGA AAATACTTCT TTGAGCTCAA CTACGAACTC CCTAATGCAA	60
TTAAATGATG ACAACAGGCT CTACAGTAAT GACTTTAACT CCGGAGAAGC TAACACTTCT	120
GATGCATTTA ACTGGACAGT CGACTCTGAA AATCGAACCA ACCTTTCCTG TGAAGGGTGC	180
CTCTCACCGT CGTGTCTCTC CTTACTTCAT CTCCAGGAAA AAAACTGGTC TGCTTTACTG	240
ACAGCCGTAG TGATTATTCT AACTATTGCT GGAAACATAC TCGTCATCAT GGCAGTGTCC	300
CTAGAGAAAA AGCTGCAGAA TGCCACCAAC TATTTCTCTGA TGTCACTTGC CATAGCTGAT	360
ATGCTGCTGG GTTTCCTTGT CATGCCCCGTG TCCATGTTAA CCATCCTGTA TGGGTACCGG	420
TGGCCTCTGC CGAGCAAGCT TTGTGCAGTC TGGATTTACC TGGACGTGCT CTTCTCCACG	480
GCCTCCATCA TGCACCTCTG CGCCATCTCG CTGGACCGCT ACGTCGCCAT CCAGAATCCC	540
ATCCACCACA GCCGCTTCAA CTCCAGAACT AAGGCATTTT TGAATATCAT TGCTGTTTGG	600
ACCATATCAG TAGGTATATC CATGCCAATA CCAGTCTTTG GGCTACAGGA CGATTCTGAAG	660
GTCTTTAAGG AGGGGAGTTG CTTACTCGCC GATGATAACT TTGTCCTGAT CGGCTCTTTT	720
GTGTCATTTT TCATTCCCCT GACGATTATG GTGATTACGT ATTGCCTGAC CATCTACGTT	780
CTGCGCCGAC AAGCTTTGAT GTTACTGCAC GGCCACACCG AGGAACCGCC TGGACTAAGT	840
CTGGATTTCC TGAAGTGCTG CAAGAGGAAT ACGGCCGAGG AAGAGAACTC TGCAAACCCCT	900
AACCAAGACC AGAACGCACG CCGAAGAAAG AAGAAGGAGA GACGTCCTAG GGGCACCATG	960
CAGGCTATCA ACAATGAAAG AAAAGCTAAG AAAGTCCTTG GGATTGTTTT CTTTGTGTTT	1020
CTGATCATGT GGTGCCCTTT CTTTCATCACA AACATCATGG CCGTCATCTG CAAAGAGTCC	1080
TGCAATGAGG ATGTCATTGG GGCCCTGCTC AATGTGTTTG TTTGGATCGG TTATCTCTCT	1140
TCAGCAGTCA ACCCACTAGT CTATACTCTG TTCAACAAAA TTTACCGAAG GGCATTCTCC	1200
AACTATTTGC GTTGCAATTA TAAGGTAGAG AAAAAGCCTC CTGTCAGGCA GATTCCAAGA	1260
GTTGCCGCCA CTGCTTTGTC TGGGAGGGAG CTTAATGTGA ACATTTATCG GCATACCAAT	1320
GAACCGGTGA TCGAGAAAGC CAGTGACAAT GAGCCCGGTA TAGAGATGCA AGTTGAGAAT	1380
TTAGAGTTAC CAGTAAATCC CTCCAGTGTG GTTAGCGAAA GGATTAGCAG TGTGTGA	1437

(34) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 478 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

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Met Asp Ile Leu Cys Glu Glu Asn Thr Ser Leu Ser Ser Thr Thr Asn
1          5          10          15
Ser Leu Met Gln Leu Asn Asp Asp Asn Arg Leu Tyr Ser Asn Asp Phe
20          25          30
Asn Ser Gly Glu Ala Asn Thr Ser Asp Ala Phe Asn Trp Thr Val Asp
35          40          45
Ser Glu Asn Arg Thr Asn Leu Ser Cys Glu Gly Cys Leu Ser Pro Ser
50          55          60
Cys Leu Ser Leu Leu His Leu Gln Glu Lys Asn Trp Ser Ala Leu Leu
65          70          75          80
Thr Ala Val Val Ile Ile Leu Thr Ile Ala Gly Asn Ile Leu Val Ile
85          90          95
Met Ala Val Ser Leu Glu Lys Lys Leu Gln Asn Ala Thr Asn Tyr Phe
100         105         110
Leu Met Ser Leu Ala Ile Ala Asp Met Leu Leu Gly Phe Leu Val Met
115         120         125
Pro Val Ser Met Leu Thr Ile Leu Tyr Gly Tyr Arg Trp Pro Leu Pro
130         135         140
Ser Lys Leu Cys Ala Val Trp Ile Tyr Leu Asp Val Leu Phe Ser Thr
145         150         155         160
Ala Ser Ile Met His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala
165         170         175
Ile Gln Asn Pro Ile His His Ser Arg Phe Asn Ser Arg Thr Lys Ala
180         185         190
Phe Leu Lys Ile Ile Ala Val Trp Thr Ile Ser Val Gly Ile Ser Met
195         200         205
Pro Ile Pro Val Phe Gly Leu Gln Asp Asp Ser Lys Val Phe Lys Glu
210         215         220
Gly Ser Cys Leu Leu Ala Asp Asp Asn Phe Val Leu Ile Gly Ser Phe
225         230         235         240
Val Ser Phe Phe Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Cys Leu
245         250         255
Thr Ile Tyr Val Leu Arg Arg Gln Ala Leu Met Leu Leu His Gly His
260         265         270
Thr Glu Glu Pro Pro Gly Leu Ser Leu Asp Phe Leu Lys Cys Cys Lys
275         280         285
Arg Asn Thr Ala Glu Glu Glu Asn Ser Ala Asn Pro Asn Gln Asp Gln

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290	295	300
Asn Ala Arg Arg Arg Lys Lys Lys Glu Arg Arg Pro Arg Gly Thr Met 305 310 315 320		
Gln Ala Ile Asn Asn Glu Arg Lys Ala Lys Lys Val Leu Gly Ile Val 325 330 335		
Phe Phe Val Phe Leu Ile Met Trp Cys Pro Phe Phe Ile Thr Asn Ile 340 345 350		
Met Ala Val Ile Cys Lys Glu Ser Cys Asn Glu Asp Val Ile Gly Ala 355 360 365		
Leu Leu Asn Val Phe Val Trp Ile Gly Tyr Leu Ser Ser Ala Val Asn 370 375 380		
Pro Leu Val Tyr Thr Leu Phe Asn Lys Ile Tyr Arg Arg Ala Phe Ser 385 390 395 400		
Asn Tyr Leu Arg Cys Asn Tyr Lys Val Glu Lys Lys Pro Pro Val Arg 405 410 415		
Gln Ile Pro Arg Val Ala Ala Thr Ala Leu Ser Gly Arg Glu Leu Asn 420 425 430		
Val Asn Ile Tyr Arg His Thr Asn Glu Pro Val Ile Glu Lys Ala Ser 435 440 445		
Asp Asn Glu Pro Gly Ile Glu Met Gln Val Glu Asn Leu Glu Leu Pro 450 455 460		
Val Asn Pro Ser Ser Val Val Ser Glu Arg Ile Ser Ser Val 465 470 475		

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/08168

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C07H 21/04; C07K 14/705; C12N 15/09, 15/63; C12Q 1/68
US CL : 536/23.5, 24.3; 435/7.1, 69.1, 320.1; 530/350

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.5, 24.3; 435/7.1, 69.1, 320.1; 530/350

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, MEDLINE, HCAPLUS, BIOSIS, EMBASE, JAPIO, WPIDS

search terms: serotonin receptor, 5ht2, agonist, antagonist, inverse agonist, chemical structure of compound A, B, i, II, III.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	HARTMAN, J.L. et al. Functional Reconstitution in Situ of 5-Hydroxytryptamine 2c (5HT2c) Receptors with Alpha-q and Inverse Agonism of 5HT2c Receptor Antagonists. J. Biol. Chem. 13 September 1996, Vol. 271, No. 37, pages 22591-22597, see entire document.	7
A,P	WO 98/24785 A1 (FUGI-SAWA PHARMACEUTICAL CO., LTD.) 11 June 1998, see entire document.	7, 18, 19

☐

Further documents are listed in the continuation of Box C.

☐

See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	* & * document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

26 JULY 1999

Date of mailing of the international search report

28 AUG 1999

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

NIRMAL S. BASI

Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US99/08168

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 1-6, 8-10 and 15-17
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

Claims 1-6 and 8-10 require a sequence search of the amino acid sequence of the protein or nucleotide search of the polynucleotide. The sequences in computer readable form were defective. Claims 15-17 are not present in the application.
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
7, 18 and 19
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐

The additional search fees were accompanied by the applicant's protest.

☐

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/08168

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claim(s)7, drawn to a method for identifying whether a candidate compound is an inverse agonist to a non-endogenous human 5HT2 serotonin receptor.

Group II, claim(s) 11, drawn to an agonist to a non-endogenous human 5HT2 serotonin receptor.

Group III, claim(s) 12 and 13, drawn to a reagent for screening compounds to determine whether the compounds are inverse agonists to human 5HT2 serotonin receptor.

Group IV, claim(s)14, drawn to a method for modulating by inverse agonism the activity of a human 5HT2a serotonin receptor by contacting the receptor with the compound A.

Group V, claim(s) 18, drawn to a method for modulating by inverse agonism the activity of a human 5HT2a serotonin receptor by contacting the receptor with the compound B.

Group VI, claim(s) 19, drawn to a method for modulating by inverse agonism the activity of a human 5HT2a serotonin receptor by contacting the receptor with the compound I.

Group VII, claim(s)20, drawn to a method for modulating by inverse agonism the activity of a human 5HT2a serotonin receptor by contacting the receptor with the compound II.

Group VIII, claim(s) 20, drawn to a method for modulating by inverse agonism the activity of a human 5HT2a serotonin receptor by contacting the receptor with the compound III.

Group IX, claim(s) 21 and 22, drawn to compound C and use for manufacture of a medicament.

Claims 15-17 are not grouped because they were not present in the application.

The inventions listed as Groups I-IX do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: The special technical feature of Group I is the method for identifying whether a candidate compound is an inverse agonist to a non-endogenous human 5HT2 serotonin receptor. Pursuant 37 CFR 1.474 (d), the claim is considered by the ISA/US to constitute the main invention, and none of the related Groups I-IX correspond to the main invention. Prior art teaches the special technical feature of Group I. Hartman et al (J. Biol. Chem., 1996, Vol. 271, No.3, pages 22591-22597) disclose a method for identifying whether a candidate compound is an inverse agonist to a non-endogenous human 5HT2 serotonin receptor. The method of Group I does not provide an advance over the prior art. The methods of Groups IV-VIII do not share a special technical feature in any pairing because the special technical feature is the inverse agonist, and each method is practiced by a different inverse agonist. The products of Groups II, III and IX do not share the technical feature in any pairing because the compounds are structurally different and capable of separate use and manufacture.